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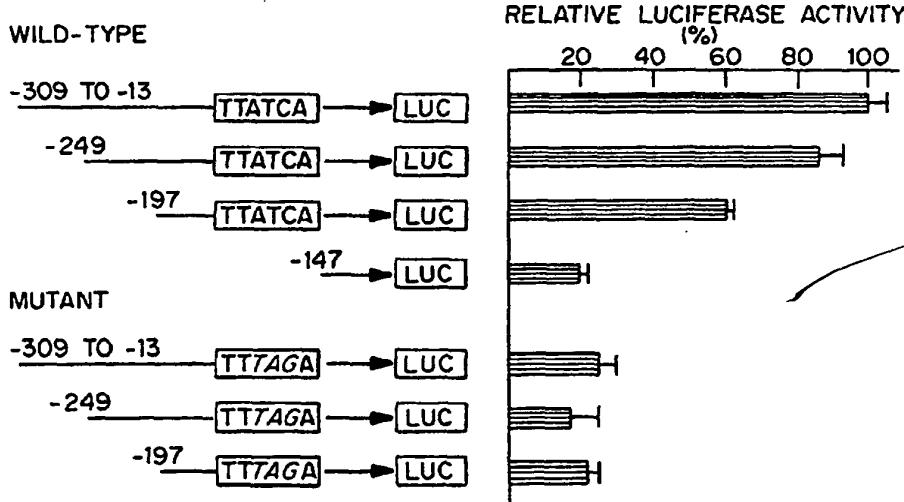
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(54) Title: EXPRESSION CONTROL SEQUENCES OF THE P-SELECTIN GENE



(57) Abstract

DNA molecules and methods for the regulated expression of a gene in endothelial cells or megakaryocytes, are described, wherein the 5' flanking region of the P-selectin gene, or portions thereof, is ligated to the 5' end of a gene. The DNA molecules are also used as probes for screening individuals with abnormal levels of expression of P-selectin, or for production of pharmaceutical compositions to inhibit inflammation by inhibition of expression of P-selectin. These DNA molecules can also be used to identify and isolate previously unknown proteins which are involved in regulation of gene expression.

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EXPRESSION CONTROL SEQUENCES OF THE P-SELECTIN GENE

Background of the Invention

This invention is generally in the field of compositions and methods for the treatment and prevention of inflammatory responses involving P-selectin (formerly, GMP-140 or PADGEM) binding reactions, particularly adhesive interactions between platelets, leukocytes, and endothelial cells.

The adherence of leukocytes to vascular surfaces is a critical component of the inflammatory response, and is part of a complex series of reactions involving the simultaneous and interrelated activation of the complement, coagulation, and immune systems. Leukocyte adherence to vascular endothelium is a key initial step in migration of leukocytes to tissues in response to microbial invasion. The initial rolling contacts of leukocytes with the endothelium are mediated by the selectins, a family of receptors that interact with cell-surface carbohydrate ligands (reviewed in McEver, *Curr. Opin. Cell Biol.*, 4, pages 840-859 (1992); Lasky, *Science*, 258, pages 964-969, (1992)). These transient adhesive interactions allow time for leukocytes to become activated by signaling molecules that are released from the endothelium or the underlying tissues. Upon activation, leukocytes functionally upregulate members of the integrin family of adhesion receptors. The integrins strengthen adhesion by binding to immunoglobulin-like counter-receptors on the endothelial cell (McEver, *Curr. Opin Cell Biol.*, 4, pages 840-859 (1992)). Adhesion and signaling molecules function cooperatively to regulate leukocyte recruitment during the inflammatory response.

Leukocytes also adhere to activated platelets, through interactions of P-selectin on the activated platelet surface with carbohydrate ligands on the leukocyte surface (McEver, in Structure, Function, and Regulation of Molecules Involved in Leukocyte Adhesion, pages 135-150 (Lipsky et al., eds., Springer-Verlag, New York, 1993)). Platelet-leukocyte interactions may serve as important links between the hemostatic and inflammatory responses to tissue injury.

The coagulation and inflammatory pathways are regulated in a coordinated fashion in response to tissue damage. For example, in addition to becoming adhesive for leukocytes, activated endothelial cells express tissue factor on the cell surface and decrease their surface expression of thrombomodulin, leading to a net facilitation of coagulation reactions on the cell surface. In some cases, a single receptor can be involved in both inflammatory and coagulation processes. For example, the Mac-1 receptor on leukocytes, a member of the CD11-CD18 group, mediates phagocytosis and serves as a receptor for the degradation product of complement C3bi, is involved in one pathway of adherence of leukocytes to endothelium, mediates granulocyte aggregation, and binds coagulation Factor X.

Proteins involved in the hemostatic and inflammatory pathways are of interest for diagnostic purposes and treatment of human disorders. An example is P-selectin, formerly known as GMP-140 (granule membrane protein 140) or PADGEM, an integral membrane glycoprotein with an apparent molecular weight of 140,000 as assessed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). P-selectin contains an N-terminal lectin-like domain, followed by an

epidermal growth factor-like module, a series of consensus repeats related to those in complement-binding proteins, a transmembrane domain, and a cytoplasmic tail, as described in the parent

5 application, United States Serial No. 07/320,408, filed March 8, 1989, the teachings of which are incorporated herein. P-selectin is a member of the selectin family of adhesion receptors that mediate leukocyte interactions with vascular endothelium or
10 platelets (McEver, *Curr. Opin. Cell Biol.*, 4, pages 840-849 (1992); Lasky, *Science*, 258, pages 964-969 (1992); Bevilacqua and Nelson, *J. Clin. Invest.*, 91, pages 379-387 (1993)). The human P-selectin gene spans over 50 kilobases (kb) and contains 17
15 exons, most of which encode structurally distinct domains (Johnston et al., *J. Biol. Chem.*, 265, pages 21381-21385 (1990)).

P-selectin was first purified (as GMP-140) from human platelets by McEver and Martin, *J. Biol. Chem.*, 259, pages 9799-9804 (1984). Monoclonal and polyclonal antibodies to P-selectin were also prepared, as reported by McEver and Martin (1984) and P.E. Stenberg, et al., *J. Cell Biol.*, 101, pages 80-886 (1985). The protein is present in
25 alpha granules of resting platelets but is rapidly redistributed to the plasma membrane following platelet activation, as reported by Stenberg, et al., (1985). The presence of P-selectin in endothelial cells and its biosynthesis by these
30 cells was reported by McEver, et al., *Blood*, 70(5) Suppl. 1:355a, Abstract No. 1274 (1987). In endothelial cells, P-selectin is found in storage granules known as the Weibel-Palade bodies. When platelet or endothelial cells are activated by
35 mediators such as thrombin, the membranes of the storage granules fuse with the plasma membrane, the soluble contents of the granules are released to

the external environment, and membrane bound P-selectin is presented within seconds on the cell surface, where it mediates adhesion of neutrophils, monocytes, and subsets of lymphocytes (McEver, in 5 Structure, Function, and Regulation of Molecules Involved in Leukocyte Adhesion, pages 135-150 (Lipsky et al., eds., Springer-Verlag, New York, 1993)).

The expression of P-selectin, as observed by 10 immunohistochemistry (McEver et al., *J. Clin. Invest.*, 84, pages 92-99 (1989)) and Northern blot analysis (Johnston et al., *Cell*, 56, pages 1033-1044 (1989)), is restricted to megakaryocytes and endothelial cells. Under certain circumstances, 15 steady-state levels of mRNA and protein are increased by inflammatory mediators such as tumor necrosis factor and endotoxin (Sanders et al., *Blood*, 80, pages 795-800 (1992); Weller et al., *J. Biol. Chem.*, 267, pages 15176-15183 (1992); Hahne 20 et al., *J. Cell Biol.*, 121, pages 655-664 (1993)). Thus, an understanding of the molecular mechanisms that control transcription of the P-selectin gene may help clarify the mechanisms for gene expression in megakaryocytes and endothelial cells and for 25 regulation of leukocyte adhesion in response to tissue injury.

The promoters of several genes whose expression is restricted to endothelial cells or megakaryocytes have been partially characterized 30 (Lee et al., *J. Biol. Chem.*, 265, pages 10446-10450 (1990); Wilson et al., *Mol. Cell Biol.*, 10, pages 4854-4862 (1990); Ravid et al., *Mol. Cell Biol.*, 11, pages 6116-6127 (1991); Romeo et al., *Nature*, 344, pages 447-449 (1990); Uzan et al., *J. Biol. Chem.*, 266, pages 8932-8939 (1991)). The GATA 35 element, initially recognized in erythroid-specific promoters, plays an important role in expression of

some of these genes (Wilson et al., (1990), Romeo et al., (1990)). However, this element is not sufficient to mediate tissue-specific expression, as expression of the GATA-binding proteins does not directly correlate with expression of the genes containing GATA elements (Yamamoto et al., *Genes & Dev.*, 4, pages 1650-1662 (1990)). A functional ETS element has been identified in the megakaryocyte-specific gene for glycoprotein IIb (Prandini et al., *J. Biol. Chem.*, 267, pages 10370-10374 (1992); Lemarchandel et al., *Mol. Cell. Biol.*, 13, pages 668-676 (1993)), but this element is also found in genes expressed in other tissues (see, for example, Macleod et al., *Trends Biochem. Sci.*, 17, pages 251-256 (1992)).

It is an object of the present invention to characterize and provide DNA and RNA sequences of the 5' flanking region of the human P-selectin gene and to provide methods of using these sequences to specifically express P-selectin and other genes in endothelial cells and megakaryocytes.

It is another object of this invention to provide nucleic acid probes for screening for individuals with abnormal levels of P-selectin.

It is a further object of this invention to provide compositions and methods including the DNA or RNA sequences of the 5' flanking region of the human P-selectin gene for inhibiting or regulating P-selectin expression to control the inflammatory and hemostatic processes involving endothelial or megakaryocytic cells.

Summary of the Invention

The 5' flanking region of the P-selectin gene contains the regulatory sequences necessary for expression of P-selectin in endothelial and megakaryocytic cells. These regulatory sequences

are demonstrated to be useful to specifically express other genes in endothelial and megakaryotic cells, both *in vitro*, for example, in tissue culture, and *in vivo*, for example, in transgenic

5 animals. In addition, these regulatory sequences can be used as probes to screen for individuals with abnormal levels of P-selectin and to make pharmaceutical compositions for the regulation or inhibition of P-selection expression in individuals
10 having or predisposed to inflammation.

Furthermore, sequences of the 5' flanking region of the P-selectin gene can be used to identify and isolate previously unknown proteins which are involved in regulation of gene expression.

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Brief Description of the Drawings

Figure 1 is a schematic of the nucleotide (SEQ ID NO:3) and deduced amino acid (SEQ ID NO:4) sequence of endothelial cell P-selectin that was

20 determined from a composite of four overlapping cDNAs: lambda GMPE1-lambda GMPE4. The relative positions of each of the cDNAs are shown by the solid arrows. The dotted arrows indicate regions found in some clones, but deleted in others. The
25 numbering of the nucleotide sequence was arbitrarily started at the first base following the adapter oligonucleotide sequence of the most 5' clone. The translated amino acid sequence of the open reading frame is given in the single-letter

30 code. The initiating methionine was assigned to the first in-frame ATG sequence that agreed with the consensus sequence for initiation of translation. The stop codon is shown by the asterisk. The thin underlines show the matching
35 positions of amino acid sequences determined from the N-terminus and from 26 peptides of platelet P-selectin. The signal peptide corresponds to

positions -41 to -1. The putative transmembrane domain is heavily underlined. The cysteine residues are circled and potential asparagine-linked glycosylation sites (NXS/T) are shown by the 5 dark circles. Two potential polyadenylation signals in the 3' untranslated region are underlined and overlined.

Figure 2 is the structure of the 5' flanking region of the P-selectin gene. The map shows the 10 cloned region (scale in kb) with the positions of exons (numbered 1-3) and the bacteriophage and plasmid clones used. The region of the 5' flanking region sequenced is shown by the open box. All 15 restriction sites for the following enzymes are shown on the map: B = *Bam*HI, E = *Eco*RI, Ev = *Eco*RV, H = *Hind*III, and X = *Xba*I.

Figure 3 illustrates the strategy to identify 20 transcriptional start sites of the P-selectin gene and the primers used for primer extension studies and anchored polymerase chain reaction (PCR) and 25 the probes used for RNase protection assays.

Figure 4 shows a summary of transcriptional 30 start sites in the 5' flanking region (Seq ID No:5) of the P-selectin gene. Vertical arrowheads, vertical arrows, and horizontal arrows indicate, respectively, the positions of the transcriptional start sites determined by primer extension, RNase protection and anchored-PCR cloning. Each 35 horizontal arrow represents an independent cDNA clone obtained by anchored PCR with sequence beginning at the indicated position between nucleotides (nt) 4768 and 4842 of SEQ ID NO. 5.

Figure 5 demonstrates transient expression analysis of P-selectin gene promoter activity. On 35 the left are diagrams of the P-selectin promoter-luciferase fusion constructs. Vertical bars indicate the restriction sites used to make the

constructs. The PCR primers used to generate the shorter constructs are depicted with short arrows. The constructs are aligned with the 5' P-selectin gene sequences numbered relative to the 5 translational start site. Constructs p1339RLUC and p701RLUC have 5' flanking sequence oriented in the reverse direction. On the right is plotted the relative luciferase activity of bovine aortic endothelial cells (BAEC) transfected with each 10 construct. Activity is graphed as a percentage, with 100% equal to 24,000 light units per 25 µg of cellular protein. The data represent the means ± SD of at least three independent experiments. Duplicate transfections were performed in each 15 experiment; the variation between duplicates did not exceed 10% of the mean for the experiment.

Figure 6 demonstrates cell-specific expression of the 5' flanking sequence of the human P-selectin gene. The P-selectin-expressing BAEC and the 20 P-selectin-nonexpressing cell lines HeLa, 293, and COS-7 were transfected with the indicated constructs. Parallel transfections with the positive control plasmid pRSVLUC were simultaneously performed. Luciferase activity is 25 expressed as light units per 25 µg of cellular protein. The data represent the means ± SD of three independent experiments. Duplication transfections were performed in each experiment.

Figure 7 is the mutational analysis of the 30 GATA element. Three wild-type truncated chimeric constructs, and their three corresponding mutant constructs in which the TTATCA sequence was changed to TTTAGA, are depicted on the left of the figure. These constructs were transfected into BAEC, and 35 the luciferase activities were measured as percent relative luciferase activity. The data represent the means ± SD of three independent experiments.

Duplicate transfections were performed in each experiment; the variation between duplicates did not exceed 5% of the mean for the experiment.

Figure 8 demonstrates the binding of nuclear proteins to the regulatory sequence encompassing the GATA element. The sequences of the upper strand oligonucleotides were used as probes and competitors. The P-selectin GATA and the nonconsensus GATA are from the indicated regions of the 5' flanking sequence of the human P-selectin gene. The mutant oligonucleotide contains three nucleotide changes in the core GATA motif of the wild-type P-selectin sequence; the same changes were used in the mutant expression constructs listed in Figure 7. The endothelin-1 GATA oligonucleotide corresponds to the functional GATA element in the human endothelin-1 promoter (Wilson et al., *Mol. Cell. Biol.*, 10, pages 4854-4862 (1990)).

Figure 9 shows five different recombinant gene constructs used to make transgenic mice. Each construct contains a different portion of the 5' flanking region of the P-selectin gene fused to the lacZ gene. Arrows indicate the orientation of the portion of the 5' flanking region of the P-selectin gene fused to lacZ. Construct 2 is like Construct 1, except that the portion of the 5' flanking region of the P-selectin gene has been fused in the opposite orientation so that P-selectin gene promoter function is directed away from lacZ.

Detailed Description of the Invention**I. Isolation, cloning and characterization of the gene encoding P-selectin and regulatory sequences associated with the P-selectin gene.**

5 As used herein, unless otherwise specified, the term nucleic acid refers to DNA and the equivalent RNA.

10 Cloning of the gene for P-selectin was first reported by G.I. Johnston, R.G. Cook and R.P. McEver in Abstract 1238 Supplement II *Circulation*, 78(4) (October 1988). Oligonucleotides were prepared based on N-terminal amino acid sequencing of P-selectin peptides and used to screen a human 15 endothelial cell cDNA library. A 3.0 Kilobase (kb) clone was isolated which encoded a protein of 727 amino acids. An N-terminal domain of 158 residues containing many cysteines, lysines, and tyrosines, is followed by an EGF-type repeating domain 20 structure, and eight tandem repeats of 62 amino acids each, except for the sixth tandem repeat which has 70 amino acids. The repeats are homologous to those found in a family of proteins that include proteins regulating C3b and C4b, but 25 are unique in having six conserved cysteines per repeat instead of the typical four. These are followed by a 24 amino acid transmembrane region and a 35 amino acid cytoplasmic tail.

As reported by Johnston, et al., in Abstract 30 1218, *Blood Suppl.* 72, 327a (November 1988), the gene for P-selectin has been localized to the long arm of chromosome 1, where genes for a number of C3b/C4b regulating proteins have been mapped.

As also reported, there appears to be at least 35 two forms of the protein derived from alternative splicing of mRNA: a soluble form and a membrane or granule bound form. Both forms generally have a 186 bp insertion, encoding a ninth 62 amino acid

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tandem repeat, between the sixth and seventh tandem repeats of the sequence. The soluble protein has a deletion that removes 40 amino acids including the transmembrane region. 11
The conclusion that P-selectin serves as a receptor for the adherence of leukocytes to activated endothelial cells and platelets was based on several observations. First, the rapid appearance of P-selectin on the surface of endothelium stimulated with thrombin or histamine parallels the inducible adherence of neutrophils to endothelium stimulated with these agonists. In addition, platelets interact with neutrophils such monocytes only after activation with agonists such as thrombin which cause redistribution of P-selectin to the cell surface; platelet agonists such as ADP which do not induce degranulation and surface expression of P-selectin do not cause platelets to adhere to leukocytes. Second, in endothelium, P-selectin is concentrated in postcapillary venules, where E-selectin is concentrated. The concentration of both proteins in this region is important because postcapillary venules are the predominant sites for binding of leukocytes to platelets prior to their migration across the endothelium into the tissues. Third, purified P-selectin coated on tissue culture microtiter wells mediates specific adherence of purified neutrophils to the wells. Fourth, polyclonal and monoclonal antibodies to P-selectin block 60-90% of the adherence of neutrophils to cultured human umbilical vein endothelial cells stimulated with histamine. Fifth, the cDNA-derived amino acid sequence of P-selectin indicates that its structure is remarkably similar to that of E-selectin, an endothelial cell protein known to bind

neutrophils. Sixth, leukocytes adhere to cells transfected with P-selectin cDNA.

The following methods were used for the production and characterization of P-selectin, 5 antibodies thereto, and nucleotide sequences encoding P-selectin.

Protein Sequencing.

P-selectin was isolated and purified from human platelet membranes. On one occasion it was 10 reduced under an atmosphere of nitrogen by the addition of dithiothreitol (20 mM, final concentration) and alkylated in the presence of iodoacetamide (Bray, et al., *Proc. Natl. Acad. Sci. USA*, 83, pages 1480-1484 (1986)). It was then 15 digested with trypsin. The resultant peptides were isolated by two-step, reverse-phase, high performance liquid chromatography (HPLC) using previously described methods (Rosa, et al., *Blood*, 72:593-600 (1988)). On a second occasion, P- 20 selectin was reduced and alkylated in the presence of 50 µCi [¹⁴C]-iodoacetamide (Amersham) before unlabeled iodoacetamide was added. It was then gel-purified (Bray, et al., 1986) and electroeluted into 25 mM Tris, 192 mM glycine, pH 8.0, containing 25 0.1% Triton X-100 (Jacobs and Clad, *Anal. Biochem.*, 154, pages 583-589, 1986). One milligram of P-selectin was digested with endoglycosidase Glu-C (Boehringer-Mannheim Biochemicals) at a ratio of 1:10 %, at 37°C. After 6 hr, an equal amount of 30 protease was added and the mixture was incubated for a further 14 hr at 37°C. Peptides were isolated by reverse-phase HPLC as described by Rosa, et al., (1988), except that the initial separation on the C4 HPLC column was carried out 35 using ammonium acetate buffer and the second separation on the C18 HPLC column was carried out using trifluoroacetic acid. Fractions containing

the purified peptides were concentrated to 50 μ l and kept frozen before sequencing. Amino acid sequences were determined from the N-terminus of the intact protein and from the peptides by using a
5 gas-phase protein sequencer (Applied Biosystems Model 470A) (Rosa, et al., 1988). Cysteine residues were identified by their elution profile on the HPLC system used by the protein sequencer, and confirmed by measuring 14 C radioactivity in
10 duplicate aliquots from each sequencing cycle.

cDNA Screening.

Based upon a portion of the amino acid sequence data, two pools of a 35-mer oligonucleotide probe, designed according to codon
15 usage tables (Lathe, *J. Mol. Biol.*, 183:1-12 (1985), were synthesized. The complementary strand was used to allow hybridization to RNA by Northern blotting. Inosine was used in one position because the third base of a glycine codon showed no
20 preferential nucleotide. The sequences of the pools were: POOL 1 (SEQ ID NO. 1):

5'-GC TGT CCA CTG ICC GAG GTT GTC ACA GCG CAC AAT-3'
A A
C T
25 C

POOL 2 (SEQ ID NO. 2):

5'-GC TGT CCA CTG ICC GAG GTT GTC ACA TCT CAC AAT-3'
A C
30 C

On Northern blots, both oligonucleotide probes
35 hybridized to a 3.6 kb transcript from poly(A)⁺ RNA isolated from CHRF-288 cells, a leukemia cell line with megakaryocyte-like properties (Witte, et al., *Cancer*, 58:238-244 (1986)). Pool 2 probes hybridized more strongly and were therefore used to
40 screen a cDNA library by standard procedures (Maniatis, et al., Molecular Cloning: A Laboratory

Manual (Cold Spring Harbor Laboratory, Cold Spring Harbor, New York 1982). Approximately 1.4 million recombinant phage from an unamplified human endothelial cell lambda gt11 library (Ye, et al., 5 *J. Biol. Chem.*, 262, pages 3718-3725 (1987) were plated out on *E. coli* Y1088 at a density of 200,000 plaques per 230-mm square plate of NZCYM agar. Duplicate nylon filters (Hybond-N, Amersham) were lifted, denatured, neutralized, and incubated at 10 42°C for 24 hr in prehybridization solution containing 5x standard saline citrate (SSC) [1x SSC is 150 mM NaCl, 15 mM sodium citrate], 5x Denhardt's solution [0.02% Ficoll, 0.02% polyvinylpyrrolidone, 0.02% BSA], 0.2% SDS, and 200 15 µg/ml herring sperm DNA. The 35-mer oligonucleotide probe 2 was end-labeled with [γ -³²P]ATP by 5'-polynucleotide kinase and was added to prehybridization solution to give a specific activity of 1×10^6 cpm/ml. The filters 20 were hybridized at 42°C overnight and the final washing conditions were 2x SSC, 0.1% SDS at 52°C. Positive plaques, identified by autoradiography of filters, were rescreened twice using the same probe and purified. The positive cDNA inserts were 25 isolated from an agarose gel following digestion of phage DNA with *Sal*I or *Eco*RI. Either enzyme could be used because, during the library construction, cDNAs were ligated to adapter oligonucleotides containing a *Sal*I restriction site as well as an 30 *Eco*RI site (Ye, et al., 1987). The inserts were subcloned into pIBI20 (IBI Biotechnologies, Inc.) for restriction mapping and DNA sequencing, and into M13mp18 (New England Biolabs) for DNA sequencing. Sequencing in M13mp18 was carried out 35 by the dideoxy chain-termination procedure (Sanger, et al., *Proc. Natl. Acad. Sci. USA*, 74, pages 5463-5467 (1977)) using either modified T7 polymerase

(Sequenase from United States Biochemicals) or Klenow fragment of DNA polymerase (Bio-Rad Laboratories). Priming was performed with either the M13 universal primer or with 17-mer oligonucleotides designed from cDNA sequence. Double-stranded plasmid DNA, isolated by a standard alkaline-lysis mini-prep method (Maniatis, et al., 1982), was sequenced using the method described by Kraft, et al., *Biotechniques*, 6, pages 544-547 (1988). The plasmid templates were primed with either universal primer, reverse primer (International Biotechnologies, Inc.), or 17-mer oligonucleotides.

Isolation and Characterization of cDNA Clones.

Three clones, positive after tertiary screening, were plaque purified, and phage DNA was prepared. The inserts from the clones, designated lambdaGMPE1, lambdaGMPE2, and lambdaGMPE3, were subcloned into plasmids and sequenced. The DNA sequences of all three clones contained long open reading frames which overlapped. The translated sequence of the longest clone, lambdaGMPE1, contained an amino acid sequence which matched the N-terminal amino acid sequence of intact platelet P-selectin but which lacked an in-frame ATG, which encodes a methionine to initiate translation, 5' to this sequence.

To identify full-length cDNAs, 1.4 million recombinant phage of the now amplified endothelial-cell cDNA library were rescreened with a 1 kb *Sma*I fragment from the 5' end of lambda GMPE1. Of the 55 positive clones identified, five were purified. DNA sequence from the 5' end of one of these new clones, designated lambdaGMPE4, matched the 5' end of lambdaGMPE1, except that the first 88 bp were not found within the first 140 bp of lambdaGMPE1. Translation of the sequence of lambdaGMPE4 showed

that there was an in-frame ATG sequence beginning at nucleotide 39. The sequence of the 5' end of lambdaGMPE4 was also found in the other four clones obtained in the second screening of the cDNA library, suggesting that it was the correct sequence and that the first 140 bp of lambdaGMPE1 was a cloning artifact. As shown in Figure 1, sequence ID No.1 is a composite nucleotide sequence of the four clones, with 91% of the sequence derived from lambdaGMPE1. Sequence ID No. 2 is the predicted amino acid sequence.

The composite sequence predicts a 5' untranslated region of 38 bp, followed by an open reading frame of 2490 bp coding for a protein of 830 amino acids, then a 3' untranslated sequence of 614 bp including two potential polyadenylation signals of AATAAA and AATTAAA. The latter signal precedes a 12 bp sequence, then a poly(A)⁺ tail of 75 bp. The nucleotide sequence GxxATGG, surrounding the first in-frame ATG beginning at base 39, agrees with the consensus sequence for initiation of protein translation (Kozak, *Nucl. Acids Res.*, 12, pages 857-872 (1984)). Therefore the first amino acid was assigned to this codon.

When compared to the sequence of the other clones, there was a 186 bp segment deleted from lambda GMPE1, corresponding to nucleotides 1744 to 1929 (Sequence ID No. 1). A 120 bp deletion was also found in lambda GMPE2 and lambda GMPE3 (nucleotides 2326 to 2445). Eight single-base substitutions (confirmed by sequencing both strands of the cDNAs) were found in the first three clones. Three were silent substitutions, changing the third degenerate base of a codon. The other five produced conservative amino-acid changes.

Northern Blot Analysis.

Total RNA was prepared from the human megakaryocyte-like leukemia cell lines CHRF-288 (Witte, et al., *Cancer*, 58, pages 238-244 (1986)) and HEL (Papayannopoulou, et al., *J. Clin. Invest.*, 79, pages 859-866) (1982)), the myeloid cell line K562 (Lozzio and Lozzio, *Blood*, 45, pages 321-334 (1975)), human umbilical vein endothelial cells, the EA.hy 926 hybrid endothelial cell line (Edgell, et al., *Proc. Natl. Acad. Sci. USA*, 80, pages 3734-3737 (1983)), human platelets, and the Daudi B-cell line (Klein, et al., *Cancer Res.*, 28, pages 1300-1310 (1969)) by an acid-guanidinium-phenol-chloroform procedure (Chomczynski and Sacchi, *Anal. Biochem.*, 162:156-159 (1987)). Both HEL cells and K562 cells were treated with Phorbol myristate acetate (PMA) for 48 hr. to induce differentiation before RNA was prepared. Poly(A)⁺ RNA was isolated from total RNA by oligo-dT cellulose chromatography (Davis, et al., Basic Methods in Molecular Biology (Elsevier, New York 1986)). Total or poly(A)⁺ RNA was electrophoresed on a 1% agarose gel containing formaldehyde, then transferred to a Hybond-N nylon membrane by standard procedures (Maniatis, et al., Molecular Cloning, A Laboratory Manual (Cold Spring Harbor, NY, 1982)). The membrane was prehybridized in 5x SSC, 5x Denhardt's solution, 0.2% SDS, and 200 µg/ml herring sperm DNA for oligonucleotide probes, or in 5x Denhardt's solution, 50% formamide, 10% dextran sulfate, and 200 µg/ml herring sperm DNA for cDNA probes. Oligonucleotide probes were labeled by the procedure described above, and cDNA probes were random-labeled with a α -³²P dCTP using the Klenow fragment of DNA polymerase in a commercial kit (Boehringer-Mannheim Biochemicals). Probes were hybridized overnight at 42°C at a specific activity of at least 1×10^6

cpm/ml. The filters to which the oligonucleotides were hybridized were washed with 2x SSC, 0.5% SDS for 20-min periods at increasing temperatures up to 52°C, whereas those used with the cDNA probes were 5 washed with 0.2x SSC, 0.1% SDS at temperatures up to 60°C and were exposed to film (X-OMAT AR, Kodak) at -80°C. Molecular weight markers of lambda DNA (Boehringer-Mannheim Biochemicals), electrophoresed in parallel with the RNA samples, were visualized 10 by including labeled lambda/HindIII DNA fragments (Bethesda Research Laboratories) [5 x 10⁵ cpm/ml] in the hybridization solution.

Southern Blot Analysis.

Human placental genomic DNA (intact or 15 digested with EcoRI, BamHI, and BamHI/HindIII) were obtained from Oncor. Intact DNA was also digested with PstI, TaqI, and XbaI. Ten µg of each digested DNA was electrophoresed on a 1.5% agarose gel and transferred to a nylon membrane using a 20 modification of the procedure of Reed and Mann, *Nucl. Acids Res.*, 13, pages 7207-7221 (1985). Briefly, the gel was soaked in 0.2 M HCl for 10 minutes, rinsed four times in water, and transferred to a nylon membrane in 0.4 M NaOH 25 buffer for 1 hr, then in 20x SSC overnight. The DNA was fixed to the membrane by exposure to UV light and hybridized with cDNA as described for the Northern blot. Lambda/HindIII fragments and φX174/HaeIII fragments (Bethesda Research 30 Laboratories) were used as standards and were visualized by including randomly labeled DNA fragments of lambda and φX174 (5 x 10⁵ cpm/ml) in the hybridization solution.

Computer Analysis.

35 DNA and protein sequence were analyzed using the Genetics Computer Group software package of the University of Wisconsin (Devereux, et al.,

Nucl. Acids Res., 12, pages 387-395 (1984)). The amino acid sequence of P-selectin was compared with the published sequences of other proteins contained in the National Biomedical Research Foundation

5 (NBRF) database (Release 16.0; 3/88).

The 5' Flanking Region of the Human P-selectin Gene

The following methods were used for the isolation and characterization of the 5' flanking 10 region of the P-selectin gene.

Cells.

Human HL-60 promyelocytic cells (ATCC No. CCL240), K562 erythroid cells (ATCC No. CCL 243), HEL erythroleukemia cells (ATCC No. TIB180), and

15 Jurkat T-lymphocytes were maintained in RPMI 1640 supplemented with 10% fetal calf serum (FCS).

Human HeLa epithelioid cells (ATCC No. CCL 2), 293 human embryonal kidney cells (ATCC No. CRL 1573), and COS-7 SV40-transformed African green monkey

20 kidney cells (ATCC No. CRL 1651) were maintained in Dulbecco's Minimal Essential Medium (DMEM, high glucose) supplemented with 10% FCS. CHRF-288 human megakaryocytic cells (Witte et al., *Cancer*, 58, pages 251-256 (1986)) were maintained in Fisher's

25 medium supplemented with 20% horse serum. Human umbilical vein endothelial cells (HUVEC) and bovine aortic endothelial cells (BAEC) were cultured as previously described (Moore et al., *J. Clin.*

Invest., 79, pages 124-130 (1987)).

30 Genomic cloning and Southern blot analysis.

A human genomic clone designated EMBL3-1 was obtained by screening a human genomic DNA library with a ³²P-labeled P-selectin cDNA as described above and by Johnston et al., *J. Biol. Chem.*, 265,

35 pages 21381-21385 (1990). DNA restriction fragments derived from this clone were subcloned into the plasmid pIBI20 (IBI) for restriction enzyme mapping and DNA sequencing. All sequencing

was carried out by the chain-termination procedure (Sanger et al., *Proc. Natl. Acad. Sci. USA*, 74, pages 5463-5467 (1977)) using Sequenase (United States Biochemicals). Southern blot analysis of 5 human placenta genomic DNA was done as previously described (Johnston et al., *Cell*, 56, pages 1033-1044 (1989)) using a random-labeled probe corresponding to the 5' flanking region of the P-selectin gene from nucleotides (nt) 4405 to 4842 10 of SEQ ID NO. 5.

Determination of transcriptional start sites.

Poly(A)⁺ RNAs were prepared from cultured HUVEC, CHRF-288, HEL, and HL-60 cells by using the Fasttrack kit (Invitrogen). The poly(A)⁺ RNAs were 15 used for primer extension studies, RNase protection experiments, and anchored polymerase chain reaction (PCR) cloning. For primer extension analysis, a 27-mer primer was prepared with the sequence, 5'-TTCTGGTTGTTAGTTTCAGAGATCAGG-3' (SEQ ID NO. 6). 20 The primer was 5' end-labeled with [γ -³²P]ATP (New England Nuclear, Inc) using T4 polynucleotide kinase (Pharmacia) and purified twice through a RNase free G-25 spin column (5'-3' Inc.). The specific activity of the labeled primer was 4 x 10⁶ 25 cpm/pmol. The annealing of the primer and the extension reaction were performed as described by Mackman et al., *Proc. Natl. Acad. Sci. USA*, 87, pages 2254-2258 (1990) except that actinomycin D was not added. The reaction products were then 30 extracted with phenol/chloroform, precipitated by ethanol, and separated on a 6% sequencing gel along with a known DNA sequencing ladder.

To confirm the results obtained by primer extension analysis, RNase protection studies were 35 carried out with two different cRNA probes by the method of Cox et al., *Blood*, 77, pages 286-293 (1991). Briefly, two genomic DNA fragments

spanning the region from nt 4555 to 4842 and nt
4405 to 4842, respectively, of SEQ ID NO. 5 were
amplified by PCR and subcloned into plasmid pIBI20
which contains a T7 promoter. The insert
5 nucleotide sequences were confirmed. The
recombinant plasmids were linearized with an
appropriate restriction enzyme and the cRNA probes
were generated with T7 RNA polymerase (Promega).
The cRNA probes were then purified on a 6%
10 sequencing gel. The linearized plasmids and cRNA
probes were hybridized in 4 M guanidine thiocyanate
and 25 mM EDTA (pH 6.0) at 42°C overnight, followed
by treatment with RNase A and RNase T1 (Promega).
Analysis of the protected products was performed as
15 described for the primer extension studies.

As a definitive approach to determine the
transcriptional start sites, anchored PCR (Frohman
et al., *Proc. Natl. Acad. Sci. USA*, 85, pages 8998-
9002 (1988) was used to clone the 5' ends of a
20 number of P-selectin cDNAs. First-strand cDNA was
synthesized from 2 µg of HEL cell mRNA with the
cDNA Cyclekit (Invitrogen), containing the strong
RNA denaturant methylmercuric hydroxide (MeHgOH),
with a specific primer,
25 5'-GATGTATATCTCCACGCAGTCCTCG-3' (SEQ ID NO. 7),
which is complementary to nt 446-422 of SEQ ID NO.
3. After removing the excess primer with a
Centricon 100 spin filter (Amicon), the 3' end of
the first strand cDNA was tailed in a 30-µl volume
30 containing tailing buffer (Bethesda Research
Laboratories), 1 mM dATP, and 15 units of terminal
deoxynucleotidyl-transferase (Bethesda Research
laboratories) for 10 min at 37°C, and then heated
for 15 min at 65°C. The reaction mixture was
35 diluted to 200 µl, and 10-µl aliquots were used to
synthesize the second strand cDNA with 10 pmol of
the anchored-primer, 5'-GAATTCGAGCTCGGTACC

TTTTTTTTTTTTTTT-3' (SEQ ID NO. 8), using 2.5 units of Taq DNA polymerase (Cetus) at 72°C for 7 min. The mixture was then subjected to PCR with two additional primers to improve specific amplification and facilitate subcloning: an adaptor primer, 5'-GAATTCTG AGCTCGGTACC-3' (SEQ ID NO. 9), which corresponded to the 5' end of the anchored primer and included restriction sites for EcoRI, SacI and KpnI, and a nested primer 5'-GTCGACTCTAGAATCAGCCCAGTTCTCAGC-3' (SEQ ID NO. 10), which was complementary to nucleotides 378-395 of the cDNA sequence and included XbaI and SalI sites. PCR was performed in a Perkin-Elmer/Cetus thermal cycler; the amplification profile involved denaturation at 94°C for 1.5 min, primer annealing at 55°C for 2.5 min, and extension at 72°C for 1 min. The anchored PCR products were detected by Southern blot analysis with two ³²P-labeled internal oligonucleotides to verify the specificity of the reaction. The largest products were then subcloned into pIBI20, and plasmid inserts from 21 individual colonies were sequenced.

Construction of chimeric luciferase expression vectors.

Plasmid pOLUC (originally designated p19LUC) and pRSVLUC (DeWet et al., *Mol. Cell. Biol.*, 7, pages 725-737 (1987)) were gifts from Dr. Donald Helinski (University of California, San Diego). The parental DNA for the creation of deletion mutants was a 5-kb *Hind*III fragment inserted into pIBI20 (pGHindIII, Figure 2) that contained the 5' flanking region, first exon, and part of the first intron of the P-selectin gene. Plasmid p1339LUC in the correct orientation and p1339RLUC in reverse orientation were constructed by inserting the 1.3 kb P-selectin 5' flanking region excised by *Hinf*I from pGHindIII into the *Sma*I site of pOLUC. Plasmids p701LUC, p701RLUC, p459LUC, p309LUC,

p249LUC, p197LUC, p147LUC, p128LUC, p100LUC, and p80LUC were constructed by ligation of the respective DNA segments generated by PCR from pGHindIII into the *SmaI* site of pOLUC. Plasmid

- 5 p4863LUC was constructed in three steps: 1) ligation into the *EcoRV* and *EcoRI* sites of pBluescript II KS (Stratagene, La Jolla, CA) of the fragment from nt 4596 to 4851 of SEQ ID NO. 5 released from p309LUC with *EcoRV* and *EcoRI*; 2) 10 insertion between the *HindIII* and *EcoRV* sites of the above construct of a fragment from nt 1 to 4596 of SEQ ID NO. 5 released from pGHindIII with *HindIII* and *EcoRV*; and 3) removal by *HindIII* and *SmaI* of the sequence from nt 1 to 4851 of SEQ ID 15 NO. 5 from the above construct followed by ligation into the *HindIII* and *SmaI* sites of pOLUC. Plasmid pm309LUC, pm249LUC, and pm197LUC, each of which contained three identical mutations in the TTATCA element, were constructed by an overlap extension 20 PCR protocol (Disdier et al., *Mol. Biol. Cell*, 3, pages 309-321 (1992)). Briefly, two separate PCR products, one for each half of the hybrid product, were generated with either an antisense or sense mutated GATA oligonucleotide (described below for 25 the gel shift assay) and one outside primer. The two products were gel purified and mixed. A second PCR was then performed using the two outside primers. The PCR product was blunt-ligated into the *SmaI* site of pOLUC. All the constructs were 30 verified by sequencing the inserts and flanking sites in the plasmid.

Molecular cloning of the 5' flanking region of the P-selectin gene.

- The genomic clone EMBL3-1 encoding the 5' 35 untranslated region of P-selectin cDNA was obtained, as described above, by screening a genomic DNA library with a ³²P-labeled P-selectin cDNA (Johnston et al., *J. Biol. Chem.*, 265, pages

21381-21385 (1990)). A 5 kb HindIII fragment encoding the 5-untranslated region of the P-selectin gene, derived from genomic clone EMBL3-1,

was subcloned into pIBI20, analyzed by restriction mapping (Figure 2), and sequenced on both strands. Southern blot analysis of human genomic DNA with a labeled DNA fragment derived from this clone revealed that restriction fragments were identical in size to those in the clone, suggesting that

there was no DNA rearrangement during cloning.

Transcriptional start sites in the 5' flanking region.

To define the transcriptional start sites for the P-selectin gene, three assays were used, as shown in Figure 3.

To map transcriptional start sites by primer extension, 10 µg of poly (A⁺) RNA from HEL cells, CHRF-288 cells, or HUVEC, or 10 µg of yeast tRNA was hybridized with a 5'-end-labeled

oligonucleotide primer. After incubation with reverse transcriptase, primer-extended products were analyzed on a 6% sequencing gel. A sequence ladder of the plasmid pIBI20 was used as size markers (lanes G, A, T, and C). At least 12

extension products were seen from nt 4769 to 4839 of SEQ ID NO. 5 relative to the ATG codon initiating translation of mRNA. Extension products of the same size were produced by mRNA from HUVEC and from the megakaryocytic cell lines CHRF-288 and HEL, but not by control tRNA.

Similar results were obtained by RNase protection assay using two independent cRNA probes surrounding the first exon. The two cRNA probes produced the same protected band patterns, most of which corresponded in size to the primer extension products. Ten micrograms of poly (A⁺) RNA from HEL cells, HL-60 cells, or yeast tRNA were hybridized with each of the two different cRNA probes. After

treatment with RNase, the protected products were run on a 6% sequencing gel. RNase-protected bands corresponding to the smallest primer extension products were not observed due to the short cRNA

5 probes used. However, these short primer extension products were consistently observed, indicating that they reflected alternative transcriptional start sites rather than premature stops during reverse transcription.

10 To rule out generation of multiple bands through alternative splicing of pre-mRNAs, anchored PCR was performed to clone the 5' ends of cDNAs from HEL cell mRNA. Twenty-one clones were sequenced. The sequences of the 5' ends of these 15 cDNA clones matched the genomic sequence and corresponded in length to those predicted from the primer extension and RNase protection products.

The most abundant clones began at 4786, 4814, and 4832 (four clones each) of SEQ ID NO. 5, which 20 matched the sizes of the most prominent products determined by RNase protection and/or primer extension. These data, summarized in Figure 4, indicate that transcription of the P-selectin gene is initiated at multiple identical start sites in 25 both endothelial and megakaryocytic cells.

Structural features of the 5' flanking region.

The sequence of 4866 bp of 5' flanking region concluding with the ATG at the end of the exon 1 is shown in SEQ. ID NO:3. No canonical TATA and CCAAT 30 boxes were found in the P-selectin flanking sequence. The nucleotide sequence was not GC rich and lacked a GC box (the binding site for transcription factor Sp1) that is found in many "housekeeping" genes without TATA boxes (Reynolds 35 et al., Cell, 38, pages 275-285 (1984)). It also lacked an "initiator" sequence which is required for accurate initiation of transcription in some

TATA-less genes (Smale et al., *Cell*, 57, pages 103-113 (1989)). A number of potential regulatory elements were present, including two sites at 4707-4711 and 4105-4110 recognized by the GATA family of zinc finger transcription factors (Yamamoto et al., *Genes & Dev.*, 4, pages 1650-1662 (1990); Orkin, *Cell*, 63, pages 665-672 (1990), a CACCC (GGGTG) element at 4648-4652 frequently seen in the promoters of erythroid-expressed genes (Frampton et al., *Mol. Cell. Biol.*, 10, pages 3838-3842 (1990); Schule et al., *Nature*, 332, pages 87-90 (1988), a GGGGGTGACCCC (4646-4657 of SEQ ID No. 5) overlapping with the CACCC element that is similar to the binding sites recognized by the subunit NFKB1 (p50) of the NF- κ B/rel family (Blank et al., *Trends Biochem Sci.*, 17, pages 135-140 (1992)) and by a zinc finger nuclear protein family that includes MBP-1 and MBP-2, 10 elements beginning at 4761, 4727, 4641, 4645, 4505, 4471, 4457, 4212, 4206, and 3732 of SEQ ID NO. 5, which contain a GGAAG/A SEQ core sequence that is similar to the binding site for the ETS class of oncoproteins (Karim et al., *Genes & Dev.*, 4, pages 1451-1453 (1990)), and a TCTGGAATGTG (4747-4757 of SEQ ID NO. 5) that is related to the GT-IIC element of the SV40 enhancer (Burglin, *Cell*, 66, pages 11-12 (1991)).

II. Cell Specific Expression under the control of the 5' P Selectin Regulatory Sequence.

30 Transfection and Luciferase assay.

Plasmids used for transfections were purified by cesium chloride banding. At least two different batches of plasmids for each construct were tested for the transfections. Cells were plated on a 100 mm petri dish at a density adjusted so that they reached 70-80% confluence prior to transfection. Equal volumes of 60 μ g of test plasmid and 50 μ g of lipofectin reagent (BRL), each diluted in 2.5 ml of

OptiMEM medium (BRL), were incubated for 20 min and the resulting transfection mixture was then added to the cells. After an 8 to 12 h incubation at 37°C, the transfection medium was replaced by

- 5 complete medium for an additional 36 h and the cells were then harvested for luciferase assays in a total volume of 120 µl (DeWet et al., *Mol. Cell. Biol.*, 7, pages 725-727 (1987)). Briefly, following lysis and removal of the cell debris by 10 centrifugation, 20 µl of total cellular extracts were used for each measurement for luciferase activity. The luciferase activity for each transfection was measured three times with a Monolight 2001 luminometer. The luciferase 15 activities were normalized to the amount of protein in cellular extracts as measured by the Bradford reagent (Bio-Rad).

Preparation of cell extracts and gel shift assay.

- 20 HEL, CHRF-288, K562, Jurkat, Hela, and BAEC cell nuclear extracts were prepared as described by Dignam et al., *Nucl. Acids Res.*, 11, pages 1475-1489 (1983). Extracts from HUVEC were prepared at miniscale as described by Schreiber et al., *Nucl. Acids Res.*, 17, pages 6419 (1989). COS-7 cells 25 were transfected with a plasmid encoding human GATA-2 (Dorfman et al., *J. Biol. Chem.*, 267, pages 1279-1285 (1992)), a gift from Dr. Stuart Orkin (Harvard Medical School, Cambridge, MA), or mock- 30 transfected with the plasmid pIBI20. Extracts from GATA-2-transfected or mock-transfected COS-7 cells were prepared as described in Tsai et al., *Nature*, 339, pages 446-451 (1989). A standard gel shift assay (20 µl) contained 5,000-10,000 cpm of labeled 35 oligonucleotide, 2.5 µg of poly(dI·dC), 60 mM KCl, 4 mM Tris (pH 7.5), 12 mM Hepes, 1 mM dithiothreitol, 1 mM EDTA, 10 µg bovine serum

albumin, and 3 μ l (6 μ g) of cell extracts. Gels of 4-6% acrylamide (19:1 acrylamide/N,N'-methylenebis-acrylamide w:w) were run in 0.25 x TBE buffer (1x TBE = 0.089 M Tris, 0.089 M boric acid, and 0.002 M EDTA) at 150 V and then dried prior to autoradiography. For competition experiments, unlabeled competitor duplex DNA was added to the reaction mixture before the addition of labeled probe.

10 Transgenic Mice.

The lacZ gene was excised from pCH110 (Pharmacia-LKB) by digestion with HindIII and ApaI and ligated into the phagemid, pBluescript SK+ (Stratagene), pre-digested with the same enzymes. Constructs 1-3 were prepared by removing the 5' flanking sequences of the P-selectin gene from, respectively, p1339LUC, p1339RLUC, and p701LUC (see above), by digestion with BamHI and XbaI and inserting the sequences into pBluescript at the corresponding sites such that the 5' flanking sequence was separated from lacZ by only a few base pairs of sequence in the polylinker region of the plasmid. Constructs 4 and 5 were prepared by excising the 5' flanking sequences from p459LUC and p309LUC with HindIII and EcoRI and inserting the sequences into the same lacZ-Bluescript vector.

Each of the five plasmids was purified on cesium chloride gradients. The insert containing the P-selectin 5' flanking region fused to lacZ was released from the plasmid by digestion with BamHI and XbaI. After purification from agarose gels, the DNA insert was microinjected into the pronuclei of oocytes obtained from mating mice. The microinjected oocytes were then implanted into the infundibulum of the Fallopian tubes of pseudopregnant mice using standard techniques (Hogan et al. in Manipulating the Mouse Embryo. A

Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1986) (incorporated herein by reference). Incorporation of the transgene into offspring was determined by PCR analysis of tail-

5 vein DNA, using primers specific for the 5' flanking sequence and the lacZ sequence (Chen and Evans, *Biotechniques*, 8, 32-33 (1990)). Expression of the transgene in tissues of founder mice or their offspring was determined by a cytochemical

10 staining procedure for β -galactosidase (Sanes et al., *EMBO J.*, 5, pages 3133-3142 (1986)).

Transient expression analysis of the 5' flanking region.

To test whether the 5' flanking region of the P-selectin gene had promoter activity, chimeric constructs were prepared in which serially deleted fragments of 5' flanking sequence were inserted before a promoterless luciferase gene in the plasmid p0LUC (Figure 5). Luciferase expression was measured following transfection of the constructs into BAEC. Constructs p4863LUC, p1339LUC, p701LUC, p459LUC, p309LUC, and p249LUC promoted similar levels of luciferase activity that were significantly higher than the background amounts in p0LUC-transfected cells. Serial decreases in expression were observed following transfection with p197LUC and with p147LUC and p128LUC. Only background expression was observed following transfection with p100LUC and p80LUC.

25 These data indicate that the sequences responsible for most of the promoter activity are located between 4615 and 4861 of SEQ ID NO. 5. These data also indicate that there are at least three positive regulatory domains between 4615 and 4764 of SEQ ID NO. 5 (for example, compare p249LUC, p197LUC, p128LUC, and p100LUC). The results also show that some of the positive elements in the longer constructs were position dependent, as

p1339RLUC and p701RLUC, which contained flanking sequence in reverse orientation, expressed no more luciferase in BAEC than pOLUC.

To determine whether the constructs mediated tissue-specific expression, they were transfected into COS-7, 293, and Hela cells, which do not normally synthesize P-selectin, as shown by Figure 6. In contrast to their effects in BAEC, constructs p1339LUC, p701LUC, p459LUC, and p309LUC had only basal promoter activity in these cells, although the basal levels did exceed the background activity of mock-transfected cells or cells transfected with pOLUC. Parallel transfections with RSVLUC, a plasmid containing luciferase driven by the Rous sarcoma virus promoter, resulted in high levels of expression, indicating that the cells could be transfected. These data indicate that the flanking sequence from nt 4555 to 4851 of SEQ ID NO. 5 includes elements that can direct the regulated expression of a gene in endothelial cells.

The GATA element at 4706 of SEQ ID NO. 5 is required for optimal function of the P-selectin promoter.

Deletion of the sequence between nt 4667 and 4717 of SEQ ID NO. 5 significantly reduced luciferase expression in BAEC, as shown by Figure 5, indicating the presence of a positive regulatory element(s) in this region. To determine whether the GATA (TTATCA) element at 4706 of SEQ ID NO. 5 functioned as such a positive element, the wild-type sequence TTATCA was mutated to TTTAGA in the three constructs p309LUC, p249LUC, and p197LUC, as shown by Figure 6. When the mutant constructs were transfected into BAEC, luciferase expression in each case was reduced to the level of p147LUC, which was only 20% of that produced by p309LUC. These results indicate that the GATA element is

essential for optimal transcription of the P-selectin gene, perhaps through interactions with other regulatory sequences located between nt 4555 to 4666 of SEQ ID NO. 5.

5 Gene Expression in Megakaryocytes of Transgenic Mice Containing the P-selectin Promoter.

The use of the 5' flanking region of the P-selectin gene to direct the expression of a heterologous gene in megakaryocytes was demonstrated by analysis of transgenic mice carrying portions of the 5' flanking region of the P-selectin gene fused to the bacterial lacZ gene.

Five constructs were made in which DNA, having the sequence of nt 3525 to 4851 (or the same sequence inserted in the opposite orientation), 4163 to 4851, 4405 to 4851, or 4555 to 4851 of SEQ ID NO. 5, was fused to the 5' coding region of the lacZ gene, as described in Figure 9. Each construct was then cloned and used to prepare transgenic mice as described above. Offspring carrying the transgenes for each of the five constructs were produced from founders. An analysis of bone marrow cells from mice carrying the construct having the sequence of nt 4163 to 4851 of SEQ ID NO. 5 fused to lacZ indicated that the transgene was expressed by megakaryocytes but not by other bone marrow cells.

The above results clearly indicate that the sequences of the 5' flanking region of the P-selectin gene can specifically direct the regulated expression of a gene in endothelial and megakaryocytic cells. Accordingly, a gene can be specifically expressed in endothelial cells or megakaryocytes by ligating, or otherwise fusing (for example, by PCR), the 5' end of the coding sequence of the gene to the 3' end of a DNA sequence consisting essentially of nucleotides 1 to

4863 of SEQ ID NO. 5, or one or more of the transcriptional regulatory sequences of SEQ ID NO. 5, to yield a recombinant gene construct, and transfecting, or otherwise inserting using methods known to those skilled in the art (for example, by transgenic methods, microinjection, liposome fusion) the recombinant gene construct into endothelial cells or megakaryocytes.

It is likely that some modifications in the sequence of the 5' flanking region can be introduced into the cells without alteration in function. For example, the 5' flanking sequences of a given gene in different species may be slightly different; the differences are usually in regions not critical for function and therefore not conserved among species. It is believed that the 5' flanking sequences of the P-selectin gene in other species will also be functional in humans; this prediction is supported by the observed function of the human P-selectin flanking sequence in transgenic mice (see above).

III. The 5'-P Selectin Regulatory Sequence can be used to isolate Novel Proteins.

25 The function of the GATA element correlates with its ability to bind nuclear proteins.

To determine whether the GATA element bound nuclear proteins, a 40-bp double-stranded oligonucleotide probe encompassing this sequence was synthesized, as shown in Figure 8. The ³²P-labeled probe was incubated with nuclear extracts from various cell lines in the presence of poly (dI-dC) as a competitor for nonspecific DNA-protein interactions. The resultant complexes were separated by electrophoresis on a nondenaturing polyacrylamide gel. For example, two distinct complexes (labeled A and B, where A has the slower mobility in the gel) were observed on gels when K562 and HEL cell nuclear extracts were incubated

with end-labeled P-selectin GATA oligonucleotide. Complex formation was sequence specific, as it was prevented by addition of a 100-fold molar excess of the unlabeled GATA oligonucleotide, but not by a

5 100-fold excess of an oligonucleotide encoding a nonconsensus GATA sequence located further upstream in the P-selectin 5' flanking region. Similar complexes were formed using nuclear extracts from CHRF-288, BAEC, HUVEC, and Jurkat cells, although 10 sometimes one of the complexes was only present in relatively small amounts. Two minor complexes were also observed in the gels, but these appeared to represent proteolytic degradation products as they were noted only in nuclear extracts stored for 15 prolonged intervals.

To determine whether the GATA element was required to form the observed complexes in the gel shift assays, competition gel shift assays were carried out on HEL cell nuclear extracts with an 20 oligonucleotide encoding the GATA motif from the human endothelin-1 gene promoter and the results compared to a competition gel shift assay carried out with the oligonucleotide encoding the P-selectin GATA motif, as shown by Figure 8. The 25 results indicated that the unlabeled human endothelin-1 GATA oligonucleotide probe prevented formation of complex B, but not complex A, by the ³²P-labeled P-selectin probe containing the GATA consensus sequence. The labeled endothelin-1 probe 30 formed a complex with a mobility similar, although not identical, to complex B. Formation of this complex was prevented by addition of either the unlabeled endothelin-1 probe or the P-selectin probe.

35 These data indicate that complex B represents the interaction of a member of the GATA protein

family with the GATA consensus sequence in the P-selectin promoter.

To test whether the core GATA sequence was required for binding of nuclear proteins, a mutant oligonucleotide was synthesized (Figure 8) in which the core sequence TTATCA was converted to TTTAGA, the same changes made in the mutant constructs shown in Figure 7. HEL cell and BAEC nuclear extracts were incubated with end-labeled wild-type or mutant P-selectin GATA probe in the absence or the presence of the indicated unlabeled competitor. The results showed that a 100-fold molar excess of the unlabeled mutant probe prevented formation of complex A, but not complex B, when the labeled P-selectin GATA oligonucleotide was incubated with nuclear extracts from HEL and BAEC. Furthermore, the labeled mutant probe formed complex A, but not complex B. These data indicate that the core GATA sequence is required for formation of complex B, but not complex A.

To confirm that the consensus GATA element in the P-selectin promoter bound to a member of the GATA protein family, gel shift assays were performed with extracts from COS-7 cells transfected with an expression plasmid encoding human GATA-2. Labeled P-selectin probe was incubated with extracts from mock-transfected COS-7 cells (mock) or with COS-7 cells transfected with an expression plasmid encoding human GATA-2 (hGATA-2) in the present or absence of unlabeled P-selectin GATA, unlabeled human endothelin-1 GATA, or nonconsensus GATA oligonucleotides as competitors.

The hGATA-2-transfected COS-7 extracts, but not those from mock-transfected cells, formed a DNA-protein complex with the ³²P-labeled P-selectin GATA probe. Formation of this complex was

inhibited by addition of the unlabeled endothelin-1 GATA oligonucleotide as well as by the unlabeled P-selectin probe. These results indicate that the P-selectin GATA probe binds a member(s) of the GATA protein family.

5 Other nuclear protein binding sites.

The luciferase expression studies described above indicated that the sequences responsible for most of the P-selectin promoter activity in 10 endothelial cells are located in the sequence between nt 4615 and 4851 of SEQ ID NO. 5 and that at least three positive regulatory sequences are located between nt 4615 and 4764 of SEQ ID NO. 5. In addition to these sites, gel shift studies also 15 indicated the existence of at least three regulatory sites in a 52 base pair portion of the 5' flanking region of the P-selectin gene having the sequence from nt 4615 to 4666 of SEQ ID NO. 5. This conclusion was obtained by gel shift studies 20 of four complexes that were first observed to form between nuclear protein extracts from several cell types and a double-stranded ³²P-labeled oligonucleotide corresponding to the sequence from nt 4632 to 4672 of SEQ ID NO. 5. Starting with the 25 complex with slowest mobility in the gels, these complexes were designated as I, then a closely-spaced doublet IIa and IIb, then III. Extracts from some cell types formed some, but not all, of the complexes. For example, complex I was not 30 formed by extracts of HUVECs.

Complex I was also formed by mixing nuclear extracts with an oligonucleotide having the sequence of nt 4650 to 4669 of SEQ ID NO. 5. This sequence is not related to those of known DNA 35 regulatory elements. Complex I was formed with nuclear extracts from BAECs, but complex formation was prevented when extracts were prepared from the

same cells following stimulation with phorbol myristate acetate. These results indicate that the sequence of nt 4650 to 4669 of SEQ ID NO. 5 is bound by previously undescribed regulatory

5 protein(s).

The complexes corresponding to the IIa and IIb doublet (referred to collectively as complex II for simplicity) represent interactions of the DNA with members of the NF κ B family, a group of homodimeric

10 or heterodimeric DNA-binding proteins that help regulate expression of many genes (Blank et al.,

Trends Biochem. Sci., 17, pages 135-140 (1992).

Complex II was formed not only when nuclear extracts were mixed with the oligonucleotide having

15 the sequence of nt 4632 to 4672 of SEQ ID NO. 5,

but also when mixed with a oligonucleotide having the shorter sequence of nt 4642 to 4664 of SEQ ID NO. 5. Formation of complex II was inhibited by an unlabeled oligonucleotide having the sequence

20 CGGCTGGGGATTCCCCATCT (SEQ ID NO. 11), which contains the NF κ B element of the mouse *H-2K^b* class I major histocompatibility (MHC) promoter. Complex

formation was also inhibited by a combination of antisera to NFKB1 and NFKB2 subunits, two of the

25 subunits found in certain dimeric NF-KB proteins, but not by preimmune sera. Furthermore, the labeled oligonucleotides bound to purified

recombinant homodimers of NFKB1 and NFKB2, but not to homodimers of recombinant Rel A, another subunit

30 found in some dimeric NF-KB proteins, or to heterodimers that contain the Rel A subunit in cell extracts. Methylation interference studies

indicated that the GGGG sequence in the sense strand (nt 4646 to 4650 of SEQ ID NO. 5) and the

35 GGGG in the antisense strand (nt 4654 to 4657 of SEQ ID No. 5) participated in direct contacts with NFKB1 and NFKB2 homodimers. Furthermore, a mutant

37

oligonucleotide spanning the 4642 to 4664 sequence,
in which the CCCC sequence at 4654 to 4657 was
altered to ATAG, failed to interact with NFKB1 or
NFKB2 in gel shift assays. These results indicate
that the sequences recognized by NFKB1 and NFKB2 in
the 4642 to 4664 region are consistent with known
recognition features for members of the NF- κ B
family.

Formation of complex III required the inverted
repeat sequence of nt 4635 to 4646 of SEQ ID NO. 5.
Simultaneous mutations in both halves of the
inverted repeat changing the sequence from
CTTCCATGGAAG (nt 4635 to 4646 of SEQ ID NO. 5) to
GTTGGTTCCAAG (SEQ ID NO. 12), GTTGCTTTAAG (SEQ ID
No. 13), or CTTCCATCCAAG (SEQ ID NO. 14), abolished
complex formation. An oligonucleotide having the
sequence from nt 4626 to 4650 of SEQ ID NO. 5 also
formed complex III. The sequence requirements for
the formation of complex III indicate that one or
more members of the ETS class of transcription
factors may bind to this sequence of the 5'
(HEL, CHRF-288, K562, Jurkat, HL-60, HUVEC, BAEC,
EAhy.926, and HeLa), indicating that the
III was formed by extracts from all cells tested
transcription factor(s) interacting with the
of 4626 to 4650 of SEQ ID NO. 5 is widely
expressed. Of the known ETS proteins, ets-2 and
GABP are the most widely distributed (MacLeod et
al., Trends Biochem. Sci., 17, pages 251-256
(1992)). However, oligonucleotides encoding known
recognition sites for these proteins, that is,
TCGAGCAGGAAGTGACGTCGA (SEQ ID NO. 15) or
GGCCAAACCGAACGGATGTG (SEQ ID NO. 16) for ets-2 and
AGCTTCGGAACGGAGCGAACCGCCGATCC (SEQ ID NO. 17)
for GABP, did not prevent formation of complex III
with the labeled -238 to -214 oligonucleotide,

indicating that ets-2 and GABP are not interacting with this region in the 5' flanking region of the P-selectin gen . These results indicate that the portion of the 5' flanking region of the P-selectin gene defined by nt 4635 to 4646 of SEQ ID NO. 5 is bound by previously undescribed protein(s). Such proteins may be unidentified members of the ETS family or of other families of transcription factors.

Recently a pathway has been elucidated that connects signaling at the cell surface directly to gene activation (reviewed by Darnell, et al., *Science*, 264, pages 1415-1421 (1994); Ihle, et al., *Trends Biochem. Sci.*, 19, pages 222-227 (1994); Sato and Miyajima, *Curr. Opin. Cell Biol.*, 6, pages 174-179 (1994)). This pathway is used by the interferons and by many cytokines and growth factors, including IL-3, IL-4, IL-6, oncostatin M, and epidermal growth factor. In general, binding of ligand induces dimerization or oligomerization of its receptor that allows association with JAK kinases, which phosphorylate a tyrosine residue in a group of transcription factors known as the STATs (signal transducers and activators of transcription). The phosphorylated STATs then dimerize and migrate to the nucleus, where they bind to specific DNA elements, alone or in combination with other transcription factors, resulting in transcriptional activation. Cytokines IL-3, IL-4, IL-6, and oncostatin M induce increased levels of P-selectin mRNA in cultured human umbilical vein endothelial cells or in bovine aortic endothelial cells, as measured by Northern blotting. Transcript levels begin to increase at 7 hours and are even higher at 24 hours following stimulation with each cytokine. A review of the sequence of the 5' flanking region of the human P-

sel ctin gene revealed at least four elements that shared sequence similarity to consensus binding sites for members of the STAT protein family: nt 4453 to 4461, nt 4636 to 4645, nt 4722 to 4731, and 5 nt 4745 to 4753 of SEQ ID NO. 5. A double-stranded oligonucleotide encompassing the first putative element, consisting of the sequence from nt 4446 to 4469 of SEQ ID NO. 5, formed inducible complexes with nuclear proteins from several cell lines 10 stimulated for 30 min with interferon- γ or IL-6. Formation of these complexes was inhibited by addition of an unlabeled oligonucleotide containing the hSIE sequence, an element known to bind with high affinities to stat1 homodimers, stat3 15 homodimers, and stat1-3 heterodimers (Zhong, et al., *Science*, 264, pages 95-98 (1994)). Antibody supershift experiments confirmed that two of the complexes formed by the SEQ 18 oligonucleotide contained stat1, and the mobility of another 20 complex, elicited primarily by IL-6, suggests that it represents stat3 homodimers. The SEQ 18 element formed two additional complexes with nuclear extracts from the human megakaryocytic cell line, CHRF-288; one of these complexes was inducible by 25 treatment with IL-4 for 16 hours. Formation of the latter two complexes, which may represent binding to novel STAT proteins, was not competed with the hSIE oligonucleotide. Collectively, these data indicate that several different cytokines can 30 induce increased steady-state levels of P-selectin transcripts, and that one potential mechanism for these inducible increases may be binding of phosphorylated STAT proteins to elements in the 5' flanking region of the human P-selectin gene.

35 The gel-shift assays clearly indicate that sequences defined by nt 4650 to 4669, 4635 to 4646, and 4642 to 4664 of SEQ ID NO. 5, identify distinct

domains within in the 5' flanking region of the P-selectin gene which play a significant role in the regulation of the expression of the P-selectin gene in endothelial and megakaryocytic cells. The gel-shift assays also indicate the existence of previously unknown regulatory domains of the P-selectin gene. These distinct domains of the 5' flanking region of the P-selectin gene, defined by nt 4650 to 4669 and nt 4635 to 4646 of SEQ ID NO. 5 were sufficient to form two distinct complexes, i.e., complex I and complex III, respectively. Unlike the sequence defined by nt 4642 to 4664 of SEQ ID NO. 5, which has recognition features for proteins of the NFkB regulatory protein family, the sequences required for complex I have no obvious homology to sequences recognized by any known regulatory protein family. The sequences required to form complex III may allow binding of an unknown member of the ETS family or some other class of transcription factors. The nucleotide sequence defined by nt 4446 to 4469 of SEQ ID NO. 5 appears to bind two known STAT family members, stat1 and stat3, and may bind to additional novel members of this family. The nt 4745 to 4753 of SEQ ID NO. 5 are also candidate encompassing nt 4636 to 4645, nt 4722 to 4731, and binding sites for known or novel STAT proteins.

Accordingly, the sequences of the 5' flanking region of the P-selectin gene defined by nt 4650 to 4669 and nt 4635 to 4646 of SEQ ID NO. 5 are recognized and bound by regulatory proteins with previously undescribed features and are useful for the identification and isolation of such regulatory proteins. Sequences encompassing nt 4446 to 4469, nt 4636 to 4645, nt 4722 to 4731, and nt 4745 to 4753 of SEQ ID NO. 5 may also bind to novel members

of the STAT family of transcription factors and could be used for th identification and isolation of such proteins. For example, such sequences could be attached to resins for use in the
5 isolation of unknown DNA binding proteins by affinity chromatography. As another example, such sequences could be labeled using standard methodology and used to screen for clones expressing previously unknown regulatory proteins,
10 or functional peptides thereof, in cDNA expression libraries made from mRNA from endothelial cells, megakaryocytic cells, or other cells. Of course, any other consecutive sequence of SEQ ID NO. 5 that has been shown to define a regulatory site in the
15 5' flanking region of the P-selectin gene could similarly be used in such methods to isolate the particular regulatory protein(s) that bind that sequence using techniques described herein.

IV. Diagnostic Methods

20 The luciferase expression studies, the gel shift studies, and the lacZ transgene experiments, above, clearly demonstrate that the integrity of the 5' flanking region of the P-selectin gene is critical for gene expression in endothelial and
25 megakaryocytic cells. A disruption, deletion or other mutation in the sequence of nucleotides in this region can reduce or otherwise alter expression of the P-selectin gene, or heterologous gene properly ligated to this 5' flanking region.
30 Accordingly, the DNA sequences of the 5' flanking region of the P-selectin gene can be used as hybridization probes to detect or screen for mutations in the 5' flanking region of the P-selectin gene of individuals with abnormal levels
35 of expression of P-selectin, particularly those with elevated expression which have clinical symptoms of inflammation. In addition, DNA

molecules including the DNA sequences of the 5' flanking region of the P-selectin gene can be transcribed to yield the corresponding RNA molecules, if in the judgment of the skilled

5 practitioner it is more desirable to use RNA probes instead of DNA probes.

Calculations and empirical work by Lathe and others, Lathe, *J. Mol. Biol.*, 183, pages 1-12

10 (1985); Ikuta et al., *Nucleic Acids Res.*, 15, pages

797-811 (1987); and Sambrook et al., Molecular

Cloning, A Laboratory Manual, Second Edition, pages 11.7, 11.8 (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1989), incorporated herein by reference, have established helpful guidelines for

15 the skilled practitioner to select the length of probes most sensitive to mismatches in standard hybridization protocols. For example, to detect a

single mismatch in a specific DNA sequence of the mammalian genome by hybridization, a probe length of 14 to 20 nucleotides is recommended (see, for example, Sambrook et al., pages 11.7-11.8; Lathe, Table 6, page 10). Accordingly, DNA and RNA

molecules including DNA sequences, or the corresponding RNA sequences, which include at least 20 consecutive nucleotides of SEQ ID NO. 5, or functionally equivalent molecules, for example, obtained by hybridization under stringent conditions or substitution of specific bases followed by screening for function, for use as

25 probes in diagnostic hybridization methods to detect mutations in the 5' flanking region of the P-selectin gene of individuals with altered (for example, abnormally low or high) levels of expression of P-selectin. A whole series of 30 nucleic acid probes including nucleotide sequences consisting essentially of 14 to 20 consecutive nucleotides of SEQ ID NO. 5 can be used to detect

mutations along the entire or a portion of the 5' flanking region of the P-selectin gene.

Standard methods to isolate DNA and RNA from mammalian cells and tissues are well known in the art and can be used to prepare DNA (or RNA) for routine diagnostic screening by hybridization using the probes described herein. See, for examples of methods known to those skilled in the art which can be adapted for use herein using routine variation,

5 10 Sambrook et al., Molecular Cloning, A Laboratory Manual, Second Edition, pages 6.53-6.54 (DNA); pages 7.6-7.11 (RNA) (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1989); and Chomczynski and Sacchi, *Anal. Biochem.*, 162, pages 156-159

15 15 (1987) (RNA), the teachings of which are incorporated herein by reference. Furthermore, methods of carrying out hybridizations (for example, Southern and Northern blot methods) of nucleic acids immobilized on various supports, such

20 20 as nylon membranes or nitrocellulose filters, using DNA probes described herein labelled with some standard detectable marker, for example, by using commercially available biotinylated, chemiluminescent, fluorescent, enzyme or

25 25 radioactive labeling systems, are also routine and readily adapted to screening samples of DNA (or RNA) from individuals for alterations in the 5' flanking region of the P-selectin gene. See also, Leary et al., *Proc. Natl. Acad. Sci. USA*, 80, pages

30 30 4045-4049 (1983) (biotinylated probes); and Sambrook et al., Chapter 9 ("Analysis of Genomic DNA by Southern Hybridization"), Chapter 10 ("Preparation of Radiolabeled DNA and RNA Probes"). In addition to using membranes, the

35 35 advantages of probing nucleic acid samples immobilized to the plastic wells of microtiter plates has recently been advocated, offering

another variation of the available methods of screening DNAs or RNAs by hybridization using nucleic acid probes (see Mitsuashi et al., *Nature*, 357, pages 519-520 (1992)). One of ordinary skill

5 in the art is readily able to select from a variety of standard methods the particular conditions under which hybridizations are carried out in order to diagnostically screen DNA or RNA from individuals for alterations in the 5' flanking region of the P-selectin gene using the DNA molecules described
10 herein as probes.

V. Therapeutic Methods and Compositions

As the above luciferase expression and the lacZ transgene expression studies indicate, nucleic acid molecules containing the 5' regulatory sequences of the P-selectin gene can be inserted into endothelial or megakaryocytic cells and used to regulate or inhibit heterologous gene expression

in vivo. In the luciferase experiments, the plasmid pOLUC was used as the vector to carry and express the various recombinant 5' flanking region-luciferase gene constructs in endothelial cells.

However, other vectors, including both plasmid and eukaryotic viral vectors, may be used to express a

25 particular recombinant 5' flanking region-gene construct in endothelial or megakaryocytic cells depending on the preference and judgment of the skilled practitioner (see, for example, Sambrook et al., Chapter 16). Furthermore, a number of viral

30 and nonviral vectors are being developed that enable the introduction of nucleic acid sequences in vivo (see, for example, Mulligan, *Science*, 260, pages 926-932 (1993); United States Patent No.

4,980,286; United States Patent No. 4,868,116;

35 incorporated herein by reference). Recently, a delivery system was developed in which nucleic acid is encapsulated in cationic liposomes which can be

injected intravenously into a mammal. This system has been used to introduce DNA into the cells of multiple tissues of adult mice, including endothelium and bone marrow (see, for example, Zhu 5 et al., *Science*, 261, pages 209-211 (1993); incorporated herein by reference).

The 5' flanking sequences of the P-selectin gene can also be used to inhibit the expression of the P-selectin gene in cells and thereby affect the 10 inflammatory response. For example, an antisense RNA of all or a portion of the 5' flanking region of the P-selectin gene can be used to inhibit expression of P-selectin *in vivo*. Expression vectors (for example, retroviral expression 15 vectors) are already available in the art which can be used to generate an antisense RNA of a selected DNA sequence which is expressed in a cell (see, for example, U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286). Accordingly, DNA containing all or a 20 portion of the sequence of the 5' flanking region of P-selectin gene can be inserted into an appropriate expression vector so that upon passage into the cell, the transcription of the inserted DNA yields an antisense RNA that is complementary 25 to the mRNA transcript of the P-selectin gene normally found in the cell. This antisense RNA transcript of the inserted DNA can then base-pair with the normal mRNA transcript found in the cell and thereby prevent the mRNA from being translated. 30 It is of course necessary to select sequences of the 5' flanking region that are downstream from the transcriptional start sites for the P-selectin gene to ensure that the antisense RNA contains complementary sequences present on the mRNA. Based 35 on the transcriptional start site analysis (see above and Figure 4) sequences between 4863 and 4842 of SEQ ID NO. 5 are most likely to be transcribed.

Accordingly, the DNA to be inserted into the expression vector for antisense therapy should at least contain these sequences.

Antisense RNA can be generated *in vitro* also, and then inserted into cells. Oligonucleotides can be synthesized on an automated synthesizer (for example, Model 8700 automated synthesizer of Milligen-Bioscience, Burlington, MA or ABI Model 380B). In addition, antisense deoxyoligonucleotides have been shown to be effective in inhibiting gene transcription and viral replication (see, for example, Zamecnik et al., *Proc. Natl. Acad. Sci. USA*, 75, pages 280-284 (1978); Zamecnik et al.; *PNAS*, 83, pages 4143-4146 (1986); Wickstrom et al., *Proc. Natl. Acad. Sci. USA*, 85, pages 1028-1032 (1988); Crooke, *FASEB J.*, 7, pages 533-539 (1993). Furthermore, recent work has shown that improved inhibition of expression of a gene by antisense oligonucleotides is possible if the antisense oligonucleotides contain modified nucleotides (see, for example, Offensperger et al., *EMBO J.*, 12, pages 1257-1262 (1993) (*in vivo* inhibition of duck hepatitis B viral replication and gene expression by antisense phosphorothioate oligodeoxynucleotides); Rosenberg et al., PCT WO 93/01286 (synthesis of sulfurthioate oligonucleotides); Agrawal et al., *Proc. Natl. Acad. Sci. USA*, 85, pages 7079-7083 (1988) (synthesis of antisense oligonucleoside phosphoramidates and phosphorothioates to inhibit replication of human immunodeficiency virus-1); Sarin et al., *Proc. Natl. Acad. Sci. USA*, 85, pages 7448-7794 (1989) (synthesis of antisense methylphosphonate oligonucleotides); Shaw et al., *Nucleic Acids Res.*, 19, pages 747-750 (1991) (synthesis of 3' exonuclease-resistant oligonucleotides containing 3' terminal

phosphoroamidate modifications); incorporated herein by reference).

The sequences of the 5' flanking region of P-selectin can also be used in triple helix (triplex)

5 gene therapy. Oligonucleotides complementary to gene promoter sequences on one of the strands of the DNA have been shown to bind promoter and regulatory sequences to form local triple nucleic acid helices which block transcription of the gene
10 (see, for example, Maher et al., *Science*, 245, pages 725-730 (1989); Orson et al., *Nucl. Acids Res.*, 19, pages 3435-3441 (1991); Postal et al., *Proc. Natl. Acad. Sci. USA*, 88, pages 8227-8231 (1991); Cooney et al., *Science*, 241, pages 456-459
15 (1988); Young et al., *Proc. Natl. Acad. Sci. USA*, 88, pages 10023-10026 (1991); Duval-Valentin et al., *Proc. Natl. Acad. Sci. USA*, 89, pages 504-508 (1992); Blume et al., *Nucl. Acids Res.*, 20, pages 1777-1784 (1992); Grigoriev et al., *J. Biol. Chem.*, 267, pages 3389-3395 (1992).
20

Recently, both theoretical calculations and empirical findings have been reported which provide guidance for the design of oligonucleotides for use in oligonucleotide-directed triple helix formation
25 to inhibit gene expression. For example, oligonucleotides should generally be greater than 14 nucleotides in length to ensure target sequence specificity (see, for example, Maher et al., (1989); Grigoriev et al., (1992)). Also, many
30 cells avidly take up oligonucleotides that are less than 50 nucleotides in length (see, for example, Orson et al., (1991); Holt et al., *Mol. Cell. Biol.*, 8, pages 963-973 (1988); Wickstrom et al., *Proc. Natl. Acad. Sci. USA*, 85, pages 1028-1032
35 (1988)). To reduce susceptibility to intracellular degradation, for example, by 3' exonucleases, a free amine can be introduced to a 3' terminal

hydroxyl group of oligonucleotides without loss of sequence binding specificity (Orson et al., 1991). Furthermore, more stable triplexes are formed if any cytosines that may be present in the 5 oligonucleotide are methylated, and also if an intercalating agent, such as an acridine derivative, is covalently attached to a 5' terminal phosphate (for example, via a pentamethylene bridge); again without loss of sequence specificity 10 (Maher et al., (1989); Grigoriev et al., (1992)).

Methods to produce or synthesize oligonucleotides are well known in the art. Such methods can range from standard enzymatic digestion followed by nucleotide fragment isolation (see, for 15 example, Sambrook et al., Chapters 5, 6) to purely synthetic methods, for example, by the cyanoethyl phosphoramidite method using a Milligen or Beckman System 1Plus DNA synthesizer (see also, Ikuta et al., in *Ann. Rev. Biochem.*, 53, pages 323-356 20 (1984) (phosphotriester and phosphite-triester methods); Narang et al., in *Methods Enzymol.*, 65, pages 610-620 (1980) (phosphotriester method). Accordingly, DNA sequences of the 5' flanking 25 region of the P-selectin gene described herein can be used to design and construct oligonucleotides including a DNA sequence consisting essentially of at least 15 consecutive nucleotides of SEQ ID NO. 5, with or without base modifications or intercalating agent derivatives, for use in forming 30 triple helices specifically within the 5' flanking region of a P-selectin gene in order to inhibit expression of the gene in endothelial or megakaryocytic cells.

In addition, Rosenberg et al. (PCT WO 35 93/01286) teach the topical application of compositions including antisense oligonucleotides, generally 15-30 nucleotides in length, and

Pluronic™ (polypropylene oxide - polyethylene oxide block copolymer) gel, which is liquid at 4°C and solid at room temperature. Cells in direct contact with the gel compositions will take up the
5 antisense oligonucleotides which will then base-pair to the complementary mRNA and inhibit expression of the target gene. Other biodegradable polymers can be substituted for the pluronic™ such as the polylactic acid and polyglycolic acid
10 copolymers, polyethylene, and polyorthoesters which can be used to form implants for controlled release of the nucleic acid directly to a tissue where expression is desired.

Compositions including Pluronic™ gel and the
15 antisense oligonucleotides or oligonucleotides complementary to one of the strands of the 5' flanking region (for triplex formation) can be delivered locally to the endothelial cells in blood vessels by using a catheter which is advanced into
20 a vessel and applying the composition directly to the endothelial tissue. Other means of delivering such compositions locally to cells include using infusion pumps (for example, from Alza Corporation, Palo Alto, California) or incorporating the
25 compositions into polymeric implants (see, for example, P. Johnson and J.G. Lloyd-Jones, eds., Drug Delivery Systems (Chichester, England: Ellis Horwood Ltd., 1987), which can effect a sustained release of therapeutic compositions to the
30 immediate area of the implant.

Inhibition of Inflammation by inhibition of P-selectin expression.

The above methods and compositions may be used locally or systemically to inhibit the expression
35 of P-selectin *in vivo* and thereby inhibit inflammation. The ability to inhibit or otherwise regulate the inflammatory response at a site is desirable therapeutically because an inflammatory

response may cause damage to the host if unchecked, since leukocytes release many toxic molecules that can damage normal tissues. These molecules include proteolytic enzymes and free radicals. Examples of

- 5 pathological situations in which leukocytes can cause tissue damage include injury from ischemia and reperfusion, bacterial sepsis and disseminated intravascular coagulation, adult respiratory distress syndrome, tumor metastasis, and
10 atherosclerosis. Systemic administration of compounds to achieve chronic systemic down-regulation of P-selectin expression may also be useful, for example, in a chronic disorder such as rheumatoid arthritis.

- 15 There are a number of other common clinical disorders in which ischemia and reperfusion results in organ injury mediated by adherence of leukocytes to vascular surfaces, including strokes; mesenteric and peripheral vascular disease; organ
20 transplantation; and circulatory shock (in this case many organs might be damaged following restoration of blood flow).

- Bacterial sepsis and disseminated intravascular coagulation often exist concurrently
25 in critically ill patients. They are associated with generation of thrombin, cytokines, and other inflammatory mediators, activation of platelets and endothelium, and adherence of leukocytes and aggregation of platelets throughout the vascular system. Leukocyte-dependent organ damage is an important feature of these conditions.

- 30 Adult respiratory distress syndrome is a devastating pulmonary disorder occurring in patients with sepsis or following trauma, which is
35 associated with widespread adherence and aggregation of leukocytes in the pulmonary circulation. This leads to extravasation of large

amounts of plasma into the lungs and destruction of lung tissue, both mediated in large part by leukocyt products.

Two related pulmonary disorders that are often 5 fatal are in immunosuppressed patients undergoing allogeneic bone marrow transplantation and in cancer patients suffering from complications that arise from generalized vascular leakage resulting from treatment with interleukin-2 treated LAK cells 10 (lymphokine-activated lymphocytes). LAK cells are known to adhere to vascular walls and release products that are presumably toxic to endothelium. Although the mechanism by which LAK cells adhere to endothelium is not known, such cells could 15 potentially release molecules that activate endothelium and then bind to endothelium by mechanisms similar to those operative in neutrophils.

Tumor cells from many malignancies (including 20 carcinomas, lymphomas, and sarcomas) can metastasize to distant sites through the vasculature. The mechanisms for adhesion of tumor cells to endothelium and their subsequent migration are not well understood, but may be similar to 25 those of leukocytes in at least some cases. The association of platelets with metastasizing tumor cells has been well described, indicating a role for platelets in the spread of some cancers.

Platelet-leukocyte interactions are believed 30 to be important in atherosclerosis. Platelets might have a role in recruitment of monocytes into atherosclerotic plaques; the accumulation of monocytes is known to be one of the earliest detectable events during atherogenesis. Rupture of 35 a fully developed plaque may not only lead to platelet deposition and activation and the

promotion of thrombus formation, but also the early recruitment of neutrophils to an area of ischemia.

Modifications and variations of the present invention, will be recognized by those skilled in the art from the foregoing detailed description. It is understood that such modifications and variations are intended to come within the scope of this invention as defined in the specification, and that this invention is not limited by the specific embodiments that have been presented by way of example.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Board of Regents of the University of Oklahoma

(ii) TITLE OF INVENTION: Expression Control Sequences of the P-Selection Gene

(iii) NUMBER OF SEQUENCES: 17

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(F) ZIP: 30309-4530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: yes

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 12

(D) OTHER INFORMATION: /function= "N is inosine."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 15
(D) OTHER INFORMATION: /function= "The nucleotide at position 15 can also be A or C."

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 28

(D) OTHER INFORMATION: /function= "The nucleotide at position 28 can also be A, T, or C."

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Johnston, G. I.

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(G) DATE: October-1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTGTCACT GNCCGAGTT GTCACAGCGC ACAAT

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
 - (iv) ANTI-SENSE: Yes

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 12
(D) OTHER INFORMATION: /function= "N is inosine."
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 15
(D) OTHER INFORMATION: /function= "The nucleotide at position 15 can also be A or C."
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 28
(D) OTHER INFORMATION: /function= "The nucleotide at position 28 can also be C."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
GCTGTCCACT GNCCGAGGT GTCACATCTC ACAAT 35
- (2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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CCCTGTATCTC TGAACTAACA ACCAGAAAG AAGTGGCAGC ATGGACTTAT CATTACAGCA 120
CAAAGCATA CTCTATGGAA ATTTCGGTA AATACTGCCA GAATCGCTAC ACAGACTTAG
TGGCCATCCA GAATAAAAT GAAATTGATT ACCTCAATAA GGTCCTACCC TACTACAGCT 180
240
300

CCTACTACTG	GATTGGGATC	CGAAAGAAC	ATAAGACATG	GACATGGGTG	GGAACCAAAA	360
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ACGAGGACTG	CGTGGAGATA	TACATCAAGA	GTCCGTCAAGC	CCCTGGCAAG	TGGAATGATG	480
AGCACTGCTT	GAAGAAAAG	CACGCATTG	GTTCACACAGC	CTCTCTGCCAG	GACATGTCCT	540
GCAGCAAAAC	AGGAGAGTC	CTCGAGACCA	TCGGGAACTA	CACTGCTCC	TGTTACCTCTG	600
GATTCTATGG	GCCAGAATGT	GAATACGTGA	GAGAGTGTGG	AGAACTTGAG	CTCCCTAAC	660
ACGTGCTCAT	GAACTGCAGC	CACCCCTCTGG	GAAACTCTTC	TTTTAACTCG	CAGTGCAGCT	720
TCCACTGCAC	TGACGGGTAC	CAAGTAATG	GGCCCAGCAA	GCTGGAATGTC	TTGGCTCTG	780
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CTGAACGAGG	AAACATGATIC	TGCCTTCATT	CTGCAAAAGC	ATTCCAGCAT	CAGTCTAGCT	900
GCAGCTTCAG	TTGTGAACAG	GGATTGCA	TAGTTGGACC	GGAAAGTGGTG	CAATGCACAG	960
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AAGCCCCAG	TGAAAGAAC	ATGGACTGTG	TTCATCCGCT	CACTGCTTT	GCCTATGGCT	1080
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CGCTGGAGAG	TCTGTCCAC	GGAAAGCATGG	ATTGCTCTCC	ATCCTTGAGA	GGGTTTCAGT	1260
ATGACACCAA	CTGTAGCTTC	CGCTGTGCTG	AAGGTTTCAT	GCTGAGAGGA	GCCGATATAG	1320
TTCGGGTGTGA	TAACTTGGGA	CAGTGGACAG	CACCAAGCCCC	AGTCTGTCAA	GCTTTGGCAGT	1380
GCCAGGATCT	CCCAAGTTCCA	AATGAGGCC	GGGTGAAC	CTCCCAACCC	TTCGGTGCCT	1440

TTAGGTACCA	GTCAGTCTGC	AGCTTCACCT	GCAATGAAAGG	CTTGCTCCTG	GTGGGAGCAA	1500
GTGTGCTACA	GTGCTTGGCT	ACTGGAACT	GGAAATTCTGT	TCCTCCAGAA	TGCCAAGCCA	1560
TTCCCTGCAC	ACCTTTGCTA	AGCCCTCAGA	ATGGAACAAAT	GACCTGTGTT	CAACCTCTTG	1620
GAAGTTCCAG	TTATAATTC	ACATGTCAAT	TCATCTGTGA	CGAGGGATAT	TCTTTGTCTG	1680
GACCAGAAG	ATTGGATTGT	ACTCGATCGG	GACGCTGGAC	AGACTCTCCC	CCAATGTGTG	1740
AAGCCATCAA	GTGCCAGAA	CTCTTGGCC	CAGGCCAGG	CAGCCTGGAT	TGTTCTGACA	1800
CTCGTGGAGA	ATTCATGTG	GGCTCCACCT	GTCAATTCTC	TTGTAACAAAT	GGCTTTAAC	1860
TGGAGGGCC	CAATAATGTG	GAATGCCAA	CTTCTGGAAAG	ATGGTCAGCT	ACTCCACCAA	1920
CCTGCAAGG	CATAGCATCA	CTTCCTACTC	CAGGGTTGCA	ATGTCAGGCC	CTCACCACTC	1980
CTGGGCAGGG	ACCATGTC	TGTTAGGCATC	ATCCGGAAAC	CTTGGTTTT	AAATACCACTT	2040
GTTACTTTGG	CTGCAACGCT	GGATTACAC	TCATAGGAGA	CAGCACTCTC	AGCTGAGAC	2100
CTTCAGGACA	ATGGACAGCA	GTAACTCCAG	CATGGAGAGC	TGTGAAATGC	TCAGAACTAC	2160
ATGTTAAAA	GCCAATAGCG	ATGAACTGCT	CCAACCTCTG	GGGAAACCTTC	AGTTATGGAT	2220
CAATCTGCTC	TTTCCATTGT	CTAGGGGCC	AGTTACTTAA	TGGCTCTGCA	CAAACAGCAT	2280
GCCAAGAGAA	TGGCCACTGG	TCAACTACCG	TGCCAAACTG	CCAAGCAGGA	CCATTGACTA	2340
TCCAGGAAGC	CCCTGACTTAC	TTTGTGGAG	CGGTGGCTTC	TACAATAGGT	CTGATAATGG	2400
GTGGGACGCT	CCGGCTTTG	CTAAGAAAGC	GTTTCAGACA	AAAAGATGAT	GGGAAATGCC	2460
CCTTGAATCC	TCACAGCCAC	CTAGGAACAT	ATGGAGTTTT	TACAAACGCT	GCATTGTGACC	2520
CGAGTCCTTA	AGGTTCCAT	AAACACCCAT	GAATCAAAAGA	CATGGAATTA	CCTTAGATTAA	2580

GCTCTGGACC AGCCTGTTGG ACCCGCTCTG GACCAACCC T 2640
 TGGTACATC TCAAATTCTC AACCTACCAC CCCTTCCTGT CCCACCTCTT CTCTTCCTGT 2700
 AACACAGCC ACAGAAGCCA GGAGCAAATG TTTCCTGCAGT AGTCTCTGTG CTTTGACTCA 2760
 CCTGTTACTT GAATAACAG TGAAACCAAG AGACTGGAGC ATCTGACTCA CAAGAAGACC 2820
 AGACTGTGGA GAATAAAAAA TACCTCTTA TTTCCTTGATT GAAGGAAGGT TTTCTCCACT 2880
 TTGTTGGAAA GCAGGTGGCA TCTCTAATTG GAAGAAATTCT CGTAGGCATC TTCTGGAGTC 2940
 TCCAGTGGTT GCTGTTGATG AGGCCTCTTG GACCTCTGT CTGAGGCTTC CAGAGTCC 3000
 TCTGGATGGC ACCAGAGGCT GCAGAAGGCC AGAAATCAAG CTAGAAGGCC ACATGTCACC 3060
 GTGGACCTTC CTGCCACAG TCACTGTCCC TCAAATGACC CAAAGACCAA TATTCAAATG 3120
 CGTAATTAAA AGAATTTC CC 3142

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 830 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Asn	Cys	Gln	Ile	Ala	Ile	Leu	Tyr	Gln	Arg	Phe	Gln	Arg	Val
1			5							10	15				
Val	Phe	Gly	Ile	Ser	Gln	Leu	Leu	Cys	Phe	Ser	Ala	Leu	Ile	Ser	Glu
20			20					25		25	30				
Leu	Thr	Asn	Gln	Lys	Glu	Val	Ala	Ala	Trp	Thr	Tyr	His	Tyr	Ser	Thr
35			35					40		45					

Lys Ala Tyr Ser Trp Asn Ile Ser Arg Lys Tyr Cys Gln Asn Arg Tyr
50 55 60
Thr Asp Leu Val Ala Ile Gln Asn Lys Asn Glu Ile Asp Tyr Leu Asn
65 70 75 80
Lys Val Leu Pro Tyr Tyr Ser Ser Tyr Tyr Trp Ile Gly Ile Arg Lys
85 90 95
Asn Asn Lys Thr Trp Thr Trp Val Gly Thr Lys Lys Ala Leu Thr Asn
100 105 110
Glu Ala Glu Asn Trp Ala Asp Asn Glu Pro Asn Asn Lys Arg Asn Asn
115 120 125
Glu Asp Cys Val Glu Ile Tyr Ile Lys Ser Pro Ser Ala Pro Gly Lys
130 135 140
Trp Asn Asp Glu His Cys Leu Lys Lys His Ala Leu Cys Tyr Thr
145 150 155 160
Ala Ser Cys Gln Asp Met Ser Cys Ser Lys Gln Gly Glu Cys Leu Glu
165 170 175
Thr Ile Gly Asn Tyr Thr Cys Ser Cys Tyr Pro Gly Phe Tyr Gly Pro
180 185 190
Glu Cys Glu Tyr Val Arg Glu Cys Gly Glu Leu Glu Leu Pro Gln His
195 200 205
Val Leu Met Asn Cys Ser His Pro Leu Gly Asn Phe Ser Phe Asn Ser
210 215 220
Gln Cys Ser Phe His Cys Thr Asp Gly Tyr Gln Val Asn Gly Pro Ser
225 230 235 240

Lys Leu Glu Cys Leu Ala Ser Gly Ile Trp Thr Asn Lys Pro Pro Gln
245 250 255

Cys Leu Ala Ala Gln Cys Pro Pro Leu Lys Ile Pro Glu Arg Gly Asn
260 265 270

Met Ile Cys Leu His Ser Ala Lys Ala Phe Gln His Gln Ser Ser Cys
275 280 285

Ser Phe Ser Cys Glu Glu Gly Phe Ala Leu Val Gly Pro Glu Val Val
290 295 300

Gln Cys Thr Ala Ser Gly Val Trp Thr Ala Pro Ala Pro Val Cys Lys
305 310 315 320

Ala Val Gln Cys Gln His Leu Glu Ala Pro Ser Glu Gly Thr Met Asp
325 330 335

Cys Val His Pro Leu Thr Ala Phe Ala Tyr Gly Ser Ser Cys Lys Phe
340 345 350

Glu Cys Gln Pro Gly Tyr Arg Val Arg Gly Leu Asp Met Leu Arg Cys
355 360 365

Ile Asp Ser Gly His Trp Ser Ala Pro Leu Pro Thr Cys Glu Ala Ile
370 375 380

Ser Cys Glu Pro Leu Glu Ser Pro Val His Gly Ser Met Asp Cys Ser
385 390 395 400

Pro Ser Leu Arg Ala Phe Gln Tyr Asp Thr Asn Cys Ser Phe Arg Cys
405 410 415

Ala Glu Gly Phe Met Leu Arg Gly Ala Asp Ile Val Arg Cys Asp Asn
420 425 430

Leu Gly Gln Trp Thr Ala Pro Ala Pro Val Cys Gln Ala Leu Gln Cys
435 440 445
Gln Asp Leu Pro Val Pro Asn Glu Ala Arg Val Asn Cys Ser His Pro
450 455 460 465
Phe Gly Ala Phe Arg Tyr Gln Ser Val Cys Ser Phe Thr Cys Asn Glu
465 470 475 480
Gly Leu Leu Val Gly Ala Ser Val Leu Gln Cys Leu Ala Thr Gly
485 490 495
Asn Trp Asn Ser Val Pro Pro Glu Cys Gln Ala Ile Pro Cys Thr Pro
500 505 510
Leu Leu Ser Pro Gln Asn Gly Thr Met Thr Cys Val Gln Pro Leu Gly
515 520 525
Ser Ser Tyr Lys Ser Thr Cys Gln Phe Ile Cys Asp Glu Gly Tyr
530 535 540
Ser Leu Ser Gly Pro Glu Arg Leu Asp Cys Thr Arg Ser Gly Arg Trp
545 550 555 560
Thr Asp Ser Pro Pro Met Cys Glu Ala Ile Lys Cys Pro Glu Leu Phe
565 570 575
Ala Pro Glu Gln Gly Ser Leu Asp Cys Ser Asp Thr Arg Gly Glu Phe
580 585 590
Asn Val Gly Ser Thr Cys His Phe Ser Cys Asn Asn Gly Phe Lys Leu
595 600 605
Glu Gly Pro Asn Asn Val Glu Cys Thr Thr Ser Gly Arg Trp Ser Ala
610 615 620

Thr Pro Pro Thr Cys Lys Gly Ile Ala Ser Leu Pro Thr Pro Gly Leu
625 630 635 640
Gln Cys Pro Ala Leu Thr Thr Pro Gly Gln Gly Thr Met Tyr Cys Arg
645 650 655 660
His His Pro Gly Thr Phe Gly Phe Asn Thr Thr Cys Tyr Phe Gly Cys
660 665 670 675
Asn Ala Gly Phe Thr Leu Ile Gly Asp Ser Thr Leu Ser Cys Arg Pro
675 680 685 690
Ser Gly Gln Trp Thr Ala Val Thr Pro Ala Cys Arg Ala Val Lys Cys
695 700 705 710
Ser Glu Leu His Val Asn Lys Pro Ile Ala Met Asn Cys Ser Asn Leu
710 715 720 725
Trp Gly Asn Phe Ser Tyr Gly Ser Ile Cys Ser Phe His Cys Leu Glu
725 730 735 740
Gly Gln Leu Asn Gly Ser Ala Gln Thr Ala Cys Gln Glu Asn Gly
740 745 750 755
His Trp Ser Thr Thr Val Pro Thr Cys Gln Ala Gly Pro Leu Thr Ile
755 760 765 770
Gln Glu Ala Leu Thr Tyr Phe Gly Gly Ala Val Ala Ser Thr Ile Gly
770 775 780 785
Leu Ile Met Gly Gly Thr Leu Leu Ala Leu Arg Lys Arg Phe Arg
785 790 795 800
Gln Lys Asp Asp Gly Lys Cys Pro Leu Asn Pro His Ser His Leu Gly
805 810 815

Thr Tyr Gly Val Phe Thr Asn Ala Ala Phe Asp Pro Ser Pro
820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

AAGCTTCCTG TACCTGGAAT ATTAATATT TATTTCAGAT TTGGAAATT TTCAGCTAGC 60
AATCTTAAA TAGCTTCT GACCCCTTT TCCTCTATT TCTCCTTCTT AACTACTGT 120
AATGTAAACA TTAGCTCTCT TTTTAATT TTAATTAAAT TTTGTTTT ATTTCCTGAG 180
ATGCAGTCTC ACCTGTCA CCAGGCTGGA GTGCAGTGGC ATGATCTCAG CTCACTGCCA 240
CCTTTGCCCTT CTAGGTGAA GAGATTCTGC TGCCCTCAGTC TCCCCTGAG CTGGGATTAC 300
AGCATGTGCC ACAATCCCTG GCTAATTCTT TTGTATTCTT AGTAGAGACT GGTTTCACC 360
ATGTTGGTCA GGCTGGTCTT GACTCCTGAC CTAGGTGAT CCACTCACCT TGGCCTCCCA 420
AAGCGCTGG ATTATGGCAT GAGCCACTGA GTCTGGCTGA ATGTTAGCTC TCTTGATGCT 480
GTCCCCATAAA TCTTGTAGGC TTTCATCATT TCTTTTCATT CTTTTCTC CTCTCACTGT 540
ATATTTCAA AACACCTGCT TCAGTTCACCA GATTCTTCT TCTGCTTGAT CAAGTCTGCT 600
ACTGGTGATT TCTACTGCAT TTCTCACTTC ATTCAATTATA TTTTCAGCT CCAATTCTT 660
TTATGATTTC AATCTTCTG TTACATTCT TATGTTGTC ATTATTGTT TCTCTGATT 720
CACCAAAATTG TTCTCTGTG TTTCGTTCAA AGTAACGTAG CTTCCTTAAA AACAAATTATC 780

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TTGAATCCAT	TGTCAAGGCCA	TTTGTAGTAC	TCCATTTCCTT	TTGGGTCA GC	TACTGGAAA	840
TTATTGTTT	TCTTAGGTGG	TGATATTTTA	ATTGGGTTT	TCATGGTTCT	TGCTGCCTTA	900
CACTGCTGTC	TGAGCATCTGC	GTGGATCTGC	CCAATTCA	GGCTGTATGC	GCTGACTTTG	960
GTGGAGAAAT	ACCTTCTTAT	GTGGATAAT	GCGAGGATGC	TGGCTGGGTG	GGATGCAAA	1020
GTTCTGACTT	CACTAGGGC	AAAGCTGTGT	GGTCTCCATG	CAGATCTGTC	AGCTGAGGTT	1080
GGTGTAGTG	AATACTACAG	GGATCCTTAG	AGGCCAACAC	TGTGGGTATC	TACAGTGGCA	1140
ATGAGGCTGT	TGAGGTTTC	AATTGTGACA	AGTCCTCCAT	ATCCTTTT	TTCCCCACCT	1200
GGGAAGTCA	GAATGAGGAC	ATCCCTCTTG	GAATTAGGTC	TAACCTTGCAG	GCCITGCCTCCT	1260
GGTGGTGGTG	ACACTGGGT	CTGATGAAACA	GTGCCCATGG	AGTGGCCAAAG	AGCCAAGGCC	1320
TGAAGGCATGG	GCATGGCATGG	AGGGACCACA	GCACCAAGATT	CAATTGTAGC	AATGGTACCA	1380
GTGCCCAAGG	CACAGGCCATA	CTTACTATCA	CATTGATAAT	GGTGTGTAAA	ATGCAGGTAC	1440
TTATAAGCA	GCTAAGGAGC	CAGGGACTTT	ACTGCATGCC	TACCGAGAGC	TACAGTGGCT	1500
CCAGGATCCA	GGGTGTGGGC	TAGCTCTCCT	TTGGTGGCTGA	GCTGGTGA	AGAGCATGGA	1560
CAGGCACAGA	GAACCTTGA	CTCTAGGACC	CAGGGTGTTC	ACTAGCTCAC	TATAGTGTG	1620
GCTCTGGTGT	TGGAGGTGTG	GGTGTGTGA	GTACAGCCTC	AGAGACAGGG	TCTGGAGGCC	1680
AGGTGTGCAC	ATTACTACAG	CAGCTCTGGA	GTGAGAATA	TGGTTACCT	TTCTACAGTG	1740
GCTGAACCTAG	TGTCTGGAGC	AAAGACTTTC	ACAGAGAAA	CTTGGCTGG	GGTCCCAGGG	1800
GCCACAGAGC	CACAGTCCAG	AGTGTGAATA	TCTGTAGAGC	AGCCACAACT	TTTGGGGATC	1860
						1920

AGGAACACAC	ATAGAACATTG	GAGAGGTGGT	AACCCTGGCC	CCAGTCCTGG	CGAGTGCAC	1980
AATAGCTGCT	TCTTGGTGAG	GGGGTGTGAG	GGTAGTGC	ACTGTGTTTC	CCTTTTGTG	2040
ATCCTGCTAT	GGGAATGGCT	GTGGACAAA	AGATGCCAGT	GTCTCTGTG	GAGCAGGACA	2100
CTGGGGGCT	CAGTGGCTCT	GTGTACATG	ACTGACACAG	ATAGCCTACA	AATTCTTTA	2160
TTCGTAGCTA	TCTCCTGGTG	TCTCATATAT	GCCAGTCTCA	CCGGTGA	TTCATGAA	2220
ATATTCTTTC	TTTTCTCCAT	TGTGTGTT	CAAATTCTT	AAACGGCTCT	TGAGCCCCAT	2280
CCCCCAACTC	CCCACCCCTTG	TGAGGGCTAT	TITGGTTGT	GTATAACTGT	CTATGTTGT	2340
TTTTTGTG	GGGCATAAGG	CTGACATCTC	CTACTCCACC	ATCTTGCTAA	TGTCACCTGC	2400
ATAGGAATCT	TTTTATGCTT	TCCTTATATT	CACTAAATT	TAACAATATC	AAACTTAAAA	2460
ACATATGATC	AATTGAACCT	ATTAATATCA	AACTTATTAT	AAATAAGAAA	CTACAGGCT	2520
GGGCATGGTG	GCTCATGGCT	GTAATCCAA	CATTGGGA	GGCTGAGGTG	AAAGGATCAC	2580
TTGAGCCAG	GAATTCAAGG	CCAGCCTGGG	AAATATAAGAG	AGACCCATTC	TCTAGAGATT	2640
TTTTTTTTA	ATAGCCAGT	AGTGATGGCA	CACATCTATA	GTCCAGCTA	CTCAGGAGGC	2700
TGAGGTGGGA	GAATTGCTTG	AGCCCAGGAG	GTCAAGGCTG	CAGCAAGCAG	TAATCATGCC	2760
ACTGCACCTCC	AGCCTGGGCC	GCAGAGTGTGAG	ACCCCTGTCTC	AAAAAAAGAA	CCTACTAGTC	2820
TACATACCCAC	ACCTCTTCA	CCCCATCTGA	GACTATATAT	ATTCTTCTA	ACATGAGGCA	2880
ATGCCAAAAA	GAGGAGCTGG	TGAGTGAAG	TAAGAACAGA	AAGACATGGA	GGCAAGTCTT	2940
ATAGAATAAT	AGCCAACACT	AAAACCTACA	CTTAACAGCG	TGATAGGTAT	TGTTCCAAAC	3000
ACATTAATT	CATTAAATGG	TCCTTACATG	TCTATGTATT	TGGTGATTAT	TATCCTTATT	3060

ATTCACATTG	CTGAGTGTAT	TATTCTGTTG	TCATGATGCT	GATAAGAGACA	TACCCGGAGAC	3120
TGGATAACTT	ATTAaaaaaa	AAAAGTTA	ATGGACTCAC	AGTTCACGT	GGATGGGGAG	3180
TCCTCACAAAT	CATGGTAGAA	AGCaaaAGAC	ACGTCCTAAC	TGGCAGCAGG	GAAGAGAGAG	3240
AAATGAGAAC	CAAACAAAG	GGGTTCCCCC	TTATAAAACC	ATCAGCTCTC	ATGCCACTTA	3300
TTCACTACCA	TGAGAACAGT	ATGGGGAAA	CCACCCCCAT	GATTCAATGA	TCTACCAAGGT	3360
GCCTCCACAA	ACCTGTGGAA	ATTATGGGAG	CTACAATTCC	AGATGAGATT	TGGGTGGGGA	3420
CACAGCCAAA	CCACATCACT	GAGGAACATG	AGTTATAGGG	AGATTAGTAA	CGCCCCAACAC	3480
AGCTGGTAGG	TGGTGGAGCC	AGGCAGTCTG	ACTCTAGGGT	CTGGACTCTG	AACTGCATCA	3540
TGCTGCCAAG	AAGTTCCCTCA	TTTTTCCTC	TCTCTAAGTT	TCCCCTTATTTC	CCCTACAGTC	3600
ATTCCTTCAA	CAGCATTTC	TTCACCATCT	TTTCTACTTC	TACTATATAA	TTAATTTTT	3660
CTTCTGGTC	CCAAATTCCA	ACGTGCAAAT	GCAGCCTTAT	ATACCTTAAT	TCATCTTAC	3720
CTTAGACTT	TCTTCCAATG	TTTCTACTTC	ATTCCATTTC	AAATTATTC	ATGAGATGCC	3780
TATTTACAAG	CTGTAACCAT	CATGAAGTGA	ATGAAGATA	ATACCTACTA	CTGTACAATA	3840
GAATTCCAAG	AGTATAAATA	GGAGTATGG	CTTCTGACT	TGAAACTAA	TACTTGATAC	3900
TTGATTGTC	TGTCTGAGAT	CAATCTGAAA	AGTAATAATA	ATCACTAACAA	TTTGTGAGC	3960
ATCAATTGTC	GGCCAAAGTGT	CATTICAATC	ACTCTGTACA	TATTAACTCA	TTTCATCCTA	4020
CAACAAACCG	GTGAGGCCAAG	TTCTGTTATT	CTGTTTTACA	GTTGAGAAA	CAGAGGCATA	4080
GAGAGCTTAA	GTAGTTGTC	CAGTAGATAG	CCAGAAGAGG	AGCCAGGATG	GGCTCTGGGC	4140
AGTTTAACAG	CACAGCTGAA	GTCTTAACCA	CTATGCCAAC	AGCTTTTGG	TCCTACACAT	4200

CCCATGGAA GAGGAAATA AAAAGGTATC TATTGTATA CCTTTTATT TCTGATAAA 4260
 GAAGCAGAAT TCCTTCACA TGACCTATGT CTATTATA CGTCATTTCG AACTTACCA 4320
 ATAAAATTC CCAAGGCCA GAAAACTGTT AGTGGCTTT TCCATTCTTC TCTTATTTTT 4380
 TTTGTGCTAC TAATTGCTT TCTTTCCTC AGAAGGGCTGC CGGAATAGTA AACATTCAT 4440
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 ATGTTTCCA AATGTAATAC TTAAATTGG AGCTTATATC ATAATCCAAG GAAACCTTTG 4560
 TGTGTGTACT GTCCCCACAT TGCTCAGCCT GGGATATCCA GGAGTAATT ACCTTGCGCC 4620
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 CTAAGGCTGCC AACATTACTC TTGCATTATC AACATTCAA CTTCATGGG AGGGCTGTGG 4740
 TGAGTTCTG GAATGTGAAT AGGAAGTGT TTTCTAAAC AGCCTGACAC TGAGGGAGG 4800
 CAGTGAGACT GTAAGCAGTC TGGGTTGGC AGAAGGAGA AACCCAGCAG AGTCACAGAG 4860
 GAGATG 4866

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCTGGTTTG TTAGTTCAGA GATCAGG

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25

GATGTATATC TCCACCGAGT CCTTCG

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTGGAGC TCGGTACCTT TTTTTTTTTT TTTTT

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTGGAGC TCGGTACCC

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid

18

35

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACTCTA GAATCAGGCC AGTTCTCAGC

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGGCTGGGA TTCCCCATCT

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: synthetic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGGGTCCA AG

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTGGTTTA AG

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTCATCCA AG

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGAGCAGGA AGTGACGTCA A

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCCAAACCG GAAGCATGTG

- (2) INFORMATION FOR SEQ ID NO:17:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTTGGGA ACGGAAGCGG AAACCGCCGG ATCG

We claim:

1. A method for the regulated expression of a gene in endothelial cells or megakaryocytes comprising fusing the 5' end of the coding sequence of the gene to the 3' end of a DNA molecule comprising a nucleotide sequence consisting essentially of nucleotides 1 to 4863 of SEQ ID NO. 5, or portions thereof effective to control expression of a gene, to yield a recombinant gene construct; inserting the recombinant gene construct into endothelial cells or megakaryocytes; and assaying for expression of the recombinant gene inserted into the endothelial cells or megakaryocytes.

2. The method of claim 1 for the regulated expression of a gene encoding a protein wherein the 5' end of the coding sequence of the gene is fused to the 3' end of a DNA molecule comprising a nucleotide sequence of at least eight contiguous nucleotides of a sequence selected from the group consisting of nucleotides 1 to 4863, 1 to 4851, 3525 to 4851, 3525 to 4863, 3732 to 4866, 4163 to 4851, 4163 to 4863, 4206 to 4866, 4212 to 4866, 4405 to 4851, 4405 to 4863, 4446 to 4469, 4453 to 4461, 4457 to 4866, 4471 to 4866, 4505 to 4866, 4555 to 4666, 4555 to 4851, 4555 to 4863, 4615 to 4666, 4615 to 4764, 4615 to 4851, 4615 to 4861, 4615 to 4863, 4626 to 4650, 4632 to 4672, 4635 to 4646, 4636 to 4645, 4641 to 4866, 4642 to 4664, 4645 to 4866, 4646 to 4650, 4646 to 4657, 4650 to 4669, 4667 to 4863, 4667 to 4717, 4717 to 4863, 4722 to 4731, 4727 to 4866, 4747 to 4757, 4734 to 4758, 4736 to 4764, 4736 to 4863, 4745 to 4753, 4761 to 4866 of SEQ ID NO. 5, and combinations thereof.

3. The method of claim 1 wherein the gene encodes P-selectin.

4. A method for screening for defects in the 5' flanking region of the P-selectin gene of individuals comprising hybridizing nucleic acid from cells of the individuals to a nucleic acid probe molecule comprising a nucleotide sequence consisting essentially of nucleotides 1 to 4863 of SEQ ID NO. 5, or portions thereof consisting essentially of at least fourteen consecutive nucleotide bases.

5. The method of claim 4 wherein the cells are selected from the group consisting of megakaryocytes and endothelial cells.

6. The method of claim 4 wherein the probe molecule comprises a nucleotide sequence consisting essentially of sequences selected from the group consisting of any one of the sequences defined by nucleotides 1 to 4851, 3525 to 4851, 3525 to 4863, 3732 to 4866, 4163 to 4851, 4163 to 4863, 4206 to 4866, 4212 to 4866, 4405 to 4851, 4405 to 4863, 4446 to 4469, 4453 to 4461, 4457 to 4866, 4471 to 4866, 4505 to 4866, 4555 to 4666, 4555 to 4851, 4555 to 4863, 4615 to 4666, 4615 to 4764, 4615 to 4851, 4615 to 4861, 4615 to 4863, 4626 to 4650, 4632 to 4672, 4635 to 4646, 4636 to 4645, 4641 to 4866, 4642 to 4664, 4645 to 4866, 4646 to 4650, 4646 to 4657, 4650 to 4669, 4667 to 4863, 4667 to 4717, 4717 to 4863, 4722 to 4731, 4727 to 4866, 4747 to 4757, 4734 to 4758, 4736 to 4764, 4736 to 4863, 4745 to 4753, 4761 to 4866 of SEQ ID NO. 5, and combinations thereof.

7. An isolated nucleic acid molecule comprising a nucleotide sequence consisting essentially of nucleotides 1 to 4863 of SEQ ID NO. 5, or portions thereof consisting essentially of at least fourteen consecutive nucleotides of SEQ ID NO. 5.

8. The isolated nucleic acid molecule of claim 7 comprising a nucleotide sequence consisting essentially of the consecutive nucleotides of SEQ ID NO. 5 selected from the group consisting of nucleotides 1 to 4851, 3525 to 4851, 3525 to 4863, 3732 to 4866, 4163 to 4851, 4163 to 4863, 4206 to 4866, 4212 to 4866, 4405 to 4851, 4405 to 4863, 4446 to 4469, 4453 to 4461, 4457 to 4866, 4471 to 4866, 4505 to 4866, 4555 to 4666, 4555 to 4851, 4555 to 4863, 4615 to 4666, 4615 to 4764, 4615 to 4851, 4615 to 4861, 4615 to 4863, 4626 to 4650, 4632 to 4672, 4635 to 4646, 4636 to 4645, 4641 to 4866, 4642 to 4664, 4645 to 4866, 4646 to 4650, 4646 to 4657, 4650 to 4669, 4667 to 4863, 4667 to 4717, 4717 to 4863, 4722 to 4731, 4727 to 4866, 4747 to 4757, 4734 to 4758, 4736 to 4764, 4736 to 4863, 4745 to 4753, 4761 to 4866 of SEQ ID NO. 5, and combinations thereof.

9. The isolated nucleic acid molecule of claim 7 further comprising a gene, wherein the 5' end of the gene is ligated to the 3' end of the nucleic acid molecule.

10. The isolated nucleic acid molecule of claim 9 inserted into cells capable of expressing the ligated gene.

11. The isolated nucleic acid molecule of claim 10 wherein the ligated gene is inserted into the cells in an expression vehicle capable of replicating in the cells.

12. The isolated nucleic acid molecule of claim 10 wherein the ligated gene is stably incorporated into the genome of the cells.

13. The isolated nucleic acid molecule of claim 12 wherein the cells are transgenic animals.

14. The isolated nucleic acid molecule of claim 7 inserted into an expression vector.

15. The isolated nucleic acid molecule of claim 14 wherein the vector is a retroviral vector.

16. The isolated nucleic acid molecule of claim 7 further comprising a pharmaceutically acceptable carrier for administration to a person in need of treatment thereof.

17. The isolated nucleic acid molecule of claim 16 wherein the carrier is a polymeric material providing controlled release of the nucleic acid molecule.

18. The isolated nucleic acid molecule of claim 7 wherein an intercalating agent is covalently linked to a 5' terminal phosphate.

19. The isolated nucleic acid molecule of claim 18 wherein the intercalating agent is an acridine.

20. The isolated nucleic acid molecule of claim 7 wherein an amine is covalently linked to a 3' terminal hydroxyl group.

21. The isolated nucleic acid molecule of claim 7 wherein cytosine residues are methylated.

22. A method of inhibiting P-selectin expression in cells expressing P-selectin comprising inserting into the cells a nucleic acid molecule comprising a nucleotide sequence consisting essentially of at least fifteen consecutive nucleotides of SEQ ID NO. 5.

23. The method of claim 22 for the regulated expression of a gene encoding a protein wherein the 5' end of the coding sequence of the gene is fused to the 3' end of a DNA molecule comprising a nucleotide sequence consisting essentially of sequences selected from the group consisting of sequences between nucleotide 4769 and nucleotide 1 of SEQ ID No. 5.

24. The method of claim 22 comprising inserting into the cells a nucleotide sequence forming a triplex structure with any of the sequence between nucleotides 4864 and 1 of SEQ ID No. 5.

25. A method for isolating a gene transcriptional regulatory protein, or functional DNA-binding peptide portion thereof, comprising binding to the regulatory protein or peptide portion, an isolated DNA molecule comprising a nucleotide sequence of at least eight contiguous nucleotides of SEQ ID NO. 5.

26. The method of claim 25 for isolating a gene transcriptional regulatory protein, or functional DNA-binding peptide portion thereof, comprising binding to the regulatory protein or peptide portion, an isolated DNA molecule comprising a nucleotide sequence consisting essentially of sequences selected from the group consisting of nucleotides 1 to 4863, 1 to 4851, 3525 to 4851, 3525 to 4863, 3732 to 4866, 4163 to 4851, 4163 to 4863, 4206 to 4866, 4212 to 4866, 4405 to 4851, 4405 to 4863, 4446 to 4469, 4453 to 4461, 4457 to 4866, 4471 to 4866, 4505 to 4866, 4555 to 4666, 4555 to 4851, 4555 to 4863, 4615 to 4666, 4615 to 4764, 4615 to 4851, 4615 to 4861, 4615 to 4863, 4626 to 4650, 4632 to 4672, 4635 to 4646, 4636 to 4645, 4641 to 4866, 4642 to 4664, 4645 to 4866, 4646 to 4650, 4646 to 4657, 4650 to 4669, 4667 to 4863, 4667 to 4717, 4717 to 4863, 4722 to 4731, 4727 to 4866, 4747 to 4757, 4734 to 4758, 4736 to 4764, 4736 to 4863, 4745 to 4753, 4761 to 4866 of SEQ ID NO. 5, and combinations thereof.